

adi gene. Homo
Lung cancer associ

ALIGNMENTS

RESULT 1
AAQ46688
ID AAQ46688 standard; cDNA to mRNA; 1611 BP.
XX
AC AAQ46688;
XX
DT 23-DEC-1993 (first entry)
XX
DE Human pp60 c-src gene.
XX
KW Endothelial; tyrosine kinase protein; pp60 c-src; ss.
XX
OS Homo sapiens.
XX
PN WO9314193-A.
XX
PD 22-JUL-1993.
XX
PF 05-JAN-1993; 93WO-US000445.
XX
PR 06-JAN-1992; 92US-0820011.
XX
PA (UYYA) UNIV YALE.
XX
PI Bell L, Luthringer DJ, Madri JA, Warren SL;
XX
DR WPI; 1993-243209/30.
DR P-PSDB; AAR39705.
XX
PT Genetically engineered endothelial cells - which exhibit enhanced
PT cell migration, urokinase-type plasminogen activator activity,
PT and reduced mononuclear cell adhesion and fibronectin prodn

Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-07-820-011A-3
; Sequence 3, Application US/07820011A
; Patent No. 5336615
; GENERAL INFORMATION:
; APPLICANT: Bell, Leonard
; APPLICANT: Madri, Joseph A.
; APPLICANT: Warren, Stephen L.
; APPLICANT: Luthringer, Daniel J.
; TITLE OF INVENTION: Genetically Engineered
; TITLE OF INVENTION: Endothelial Cells Exhibiting Enhanced
; TITLE OF INVENTION: Migration
; TITLE OF INVENTION: and Plasminogen Activator Activity
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maurice M. Klee/
; STREET: 1951 Burr Street
; CITY: Fairfield
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06430
; COMPUTER, READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb storage
; COMPUTER: IBM PC XT
; OPERATING SYSTEM: PC-DOS/MS-DOS 2.10
; SOFTWARE: Displaywrite 3
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/820,011A
; FILING DATE: 19920106
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Klee, Maurice M.
; REGISTRATION NUMBER: 30,399
; REFERENCE/DOCKET NUMBER: LB-101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203) 255 1400
; TELEFAX: (203) 254 1101
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1611
; TYPE: NUCLEIC ACID
; STRANDEDNESS: Double
; TOPOLOGY: Linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: No
; ANTI-SENSE: No
; ORIGINAL SOURCE:
; ORGANISM: Homo sapien
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: Chromosome 20

PUBLICATION INFORMATION:

AUTHORS: Anderson, Stephen K.

AUTHORS: Gibbs, Carol P.

AUTHORS: Tanaka, Akio

AUTHORS: Kung, Hsing-Jien

AUTHORS: Fujita, Donald J.

TITLE: Human Cellular src Gene:

TITLE: Nucleotide Sequence and Derived Amino

TITLE: Acid Sequence of the Region Coding for

TITLE: the Carboxy-Terminal Two-Thirds of

TITLE: pp60c-src

JOURNAL: Molecular and Cellular Biology

VOLUME: 5

ISSUE: 5

PAGES: 1122-1129

DATE: May, 1985

PUBLICATION INFORMATION:

AUTHORS: Tanaka, Akio

AUTHORS: Gibbs, Carol P.

AUTHORS: Arthur, Richard R.

AUTHORS: Anderson, Stephen K.

AUTHORS: Kung, Hsing-Jien

AUTHORS: Fujita, Donald J.

TITLE: DNA Sequence Encoding the

TITLE: Amino-Terminal Region of the Human c-src

TITLE: Protein: Implications of Sequence

TITLE: Divergence Among src-Type Kinase

TITLE: Oncogenes

JOURNAL: Molecular and Cellular Biology

VOLUME: 7

ISSUE: 5

PAGES: 1978-1983

DATE: May, 1987

US-07-820-011A-3

Query Match 99.9%; Score 1609.4; DB 1; Length 1611;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1610; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Thu Jun 6 11:19:53 2002

us-09-44

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seq_documentation_block:

ID AAR39706 standard; Protein; 536 AA.

XX

AC AAR39706;

XX

DT 23-DEC-1993 (first entry)

XX

DE Human pp60 c-src protein.

XX

KW Endothelial; tyrosine kinase protein; pp60 c-src; ss.

XX

OS Homo sapiens.

XX

PN WO9314193-A.

XX

PD 22-JUL-1993.

XX

PF 05-JAN-1993; 93WO-US00445.

XX

PR 06-JAN-1992; 92US-0820011.

XX

PA (UYIA) UNIV YALE.

XX

PI Bell L, Luthringer DJ, Madri JA, Warren SL;

XX

DR WPI; 1993-243209/30.

DR

P-PSDB; AAR39705.

XX

PT Genetically engineered endothelial cells - which exhibit enhanced
cell migration, urokinase-type plasminogen activator activity,
and reduced mononuclear cell adhesion and fibronectin prodn

XX

PS Disclosure; Page 75-77; 91pp; English.

XX

CC The DNA encoding a portion or (more preferably) the entire pp60
c-src polypeptide (Given in AAQ46688) is used to transform endothelial
cells. Transformed cells produce increased amounts of pp60 c-src and
have improved therapeutic properties. They migrate at faster rates
than non-transformed counterparts; have an enhanced ability to
inhibit the formation of thrombi and/or dissolve thrombi once they
have formed and exhibit reduced mononuclear cell adhesion. They can
also be used to improve the success of surgical procedures such as
coronary angioplasty, heart bypass surgery, vessel graft and stent
implantation.

XX

SQ Sequence 536 AA;

alignment_scores:

Quality: 2834.00

Length: 536

Ratio: 5.287

Gaps: 0

Percent Similarity: 100.000

Percent Identity: 100.000

alignment_block:

US-09-444-711-1 x AAR39706 ..

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1 MetGlySerAsnLysSerLysProLysAspAlaSerGlnArgArgSe 17

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seq_documentation_block:

; Sequence 4, Application US/07820011A
; Patent No. 5336615

; GENERAL INFORMATION:

; APPLICANT: Bell, Leonard
; APPLICANT: Madri, Joseph A.
; APPLICANT: Warren, Stephen L.
; APPLICANT: Luthringer, Daniel J.
; TITLE OF INVENTION: Genetically Engineered
; TITLE OF INVENTION: Endothelial Cells Exhibiting Enhanced
; TITLE OF INVENTION: Migration/
; TITLE OF INVENTION: and Plasminogen Activator Activity
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maurice M. Klee
; STREET: 1951 Burr Street
; CITY: Fairfield
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06430

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 5.25 inch, 360 Kb storage
; COMPUTER: IBM PC XT
; OPERATING SYSTEM: PC-DOS/MS-DOS 2.10
; SOFTWARE: Displaywrite 3

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/820,011A
; FILING DATE: 19920106
; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Klee, Maurice M.
; REGISTRATION NUMBER: 30,399
; REFERENCE/DOCKET NUMBER: LB-101

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (203) 255 1400
; TELEFAX: (203) 254 1101

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 536 amino acids

; TYPE: AMINO ACID

; TOPOLOGY: Linear

; MOLECULE TYPE: Protein

; HYPOTHETICAL: No

; FRAGMENT TYPE: Complete Sequence

; ORIGINAL SOURCE:

; ORGANISM: Homo sapien

; PUBLICATION INFORMATION:

; AUTHORS: Anderson, Stephen K.

; AUTHORS: Gibbs, Carol P.

; AUTHORS: Tanaka, Akio

; AUTHORS: Kung, Hsing-Jien

; AUTHORS: Fujita, Donald J.

; TITLE: Human Cellular src Gene:

; TITLE: Nucleotide Sequence and Derived Amino

; TITLE: Acid Sequence of the Region Coding for

; TITLE: the Carboxy-Terminal Two-Thirds of

; TITLE: pp60c-src

; JOURNAL: Molecular and Cellular Biology

; VOLUME: 5

; ISSUE: 5

; PAGES: 1122-1129

; DATE: May, 1985

; PUBLICATION INFORMATION:

; AUTHORS: Tanaka, Akio

; AUTHORS: Gibbs, Carol P.

AUTHORS: Arthur, Richard R.
AUTHORS: Anderson, Stephen K.
AUTHORS: Kung, Hsing-Jien
AUTHORS: Fujita, Donald J.
TITLE: DNA Sequence Encoding the
TITLE: Amino-Terminal Region of the Human c-src
TITLE: Protein: Implications of Sequence
Divergence among src-Type Kinase
TITLE: Oncogenes
JOURNAL: Molecular and Cellular Biology
VOLUME: 7
ISSUE: 5
PAGES: 1978-1983
DATE: May, 1987
US-07-820-011A-4

alignment_scores:
Quality: 2834.00 Length: 536
Ratio: 5.287 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

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US-09-444-711-1 x US-07-820-011A-4

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Thu Jun 6 11:19:50 2002

us-09-444-7.

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd

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Run on: June 4, 2002, 08:26:28 ; Search time 213.19 Seconds

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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 3472872

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Maximum DB seq length: 20000000000
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Post-processing: Minimum Match 08

Database : N_Geneseq_032802:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

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4	1218.2	75.6	1759	22	AAH28357	Nucleotide sequence
5	1216.6	75.5	1602	14	AA046687	Chicken pp60 c-src
6	1058	65.7	1090	23	AA587964	DNA encoding novel
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8	811.2	50.4	2433	24	AA594859	Human DNA sequence
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25	366.2	21.5	1574	21	AAZ66794
26	346.2	21.5	1574	22	AAH11845
27	344.2	21.4	2507	16	AAQ011859
28	344.2	21.4	3527	23	AAH696966
29	344.2	21.4	7487	23	AAH922457
30	341.6	21.2	780	20	AAZ087685
31	341.6	21.2	780	22	AAH54749
32	333.6	20.7	762	22	AAH067133
33	315	19.6	2152	23	AAH592445
34	314.4	19.5	3127	23	AAH80650
35	314	19.5	3026	23	AAH922456
36	296.2	18.4	1548	20	AAH911783
37	284	17.6	7607	14	AAH049754
38	284	17.6	7607	16	AAAT03097
39	260	16.1	4515	23	ABLI97083
40	259	16.1	3653	24	ABLI99181
41	256	15.9	5520	18	AAH61865
42	252	15.6	271	19	AAV704465
43	249.6	15.5	3623	19	AAH20457
44	249.6	15.5	3780	18	AAH61864
45	239.8	14.5	1056	21	AAH18054

ALIGNMENTS

RESULT	1
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ID	AAQ46688 standard; cDNA to mRNA; 1611 BP

Human c-yes-2 gene
Human c-yes oncogene
Nucleotide sequence
DNA encoding novel
PKA substrate, SrcC
Xenopus laevis src
Xenopus laevis src
Drosophila melanog
Drosophila melanog
Drosophila melanog
DNA encoding novel
Human protein Kinase
Human protein Kinase
Breast tumour kina
DNA encoding novel
DNA encoding novel
Human src-family k
Src-family kinase
Human cDNA clone (p
DNA encoding novel
DNA encoding novel
DNA encoding novel
human SMD encoding
pTK gene LpTK-2.
Protein tyrosine-k
Drosophila melanog
Rat mucocartilag ce
c-abl gene. Homo
Human c-src1 oncog
Human c-abl oncoge
c-abl gene. Homo
lung cancer associ

AUTHORS: Arthur, Richard R.
AUTHORS: Anderson, Stephen K.
AUTHORS: Kung, Hsing-Jien
AUTHORS: Fujita, Donald J.
TITLE: DNA Sequence Encoding the
TITLE: Amino-Terminal Region of the Human c-src
TITLE: Protein: Implications of Sequence
TITLE: Divergence among src-Type Kinase
TITLE: Oncogenes
JOURNAL: Molecular and Cellular Biology
VOLUME: 7
ISSUE: 5
PAGES: 1978-1983
DATE: May, 1987
US-07-820-011A-4

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Quality: 2834.00 Length: 536
Ratio: 5.287 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

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J9-444-711-1 x US-07-820-011A-4

Align seg 1/1 to: US-07-820-011A-4 from: 1 to: 536

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17 rLeuGlnProAlaGlnAsnValHisGlnArgGlyGlyAlaPhePro 34
101 CCTCGACAGCCCGCCAGACAGCCAGCTCGCGCGCCAGCGCGCGCC 150
34 lAsrGlnThrProSerLysProAlaSerAlaAspGlnHisArgGlyPro 50
151 AGCGGCGCTTCGCGCCCGCGCGCGCGCGAGCCAGCTGTCGAGAGCT 200
51 SerAlaAlaPheAlaProAlaAlaGlnProLysLeuPheGlyGlyPh 67
201 CAACCTCTGCGACACCGCTACCTCCCCGAGAGCGCGCGCGCTGGCC 250
67 eAsnSerSerAspThrValThrSerProGlnArgAlaGlyProLeuAla 84
251 GTGAGGTGACCACTTGTGGCCCTTATGACTATGAGTACTAGACGAG 300
84 lYgIYValThrThrPheValAlaLeuThrAspTyrGlnSerArgThrGln 100
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101 ThrAspLeuSerPheLysLysGlyLysArgLeuGlnIleValAsnAsn 117
351 GGAGGAGACTGTGGCTGGCCGCTGCTGCTGCTGCTGCTGCTGCTGCT 400
117 rGlnGlyAspTyrPheLeuAlaHisSerLeuSerThrGlyGlnThrGly 134
401 ACATCCCCGCAACTACGTGGCGCCCTCGACTCCATCCAGCGTGAAG 450
134 yrlleProSerAsnTyrValAlaProSerAspSerIleGlnAlaGlnGln 150
451 TGGTATTTTGGCAAGATCACAGACGAGGATGACAGCGGTACTGCTCA 500
151 TrpTyrPheGlyLysIleThrArgArgGlnSerGlnArgLeuLeuAs 167
501 TGCAGAGAACCGAGAGGAGACTCTCTGCTGCGAGAAAGTGAACACGA 550
167 nAlaGlnAsnProArgGlyThrPheLeuValArgGlnSerGlnThrThr 184
551 AAGGTGCTACAGCTCTCAGTGTGACTTGACACAGCCAGGCGCTC 600

184 ysgIyAlaTyrCysLeuSerValSerAspPheAspAsnAlaLysGlyLeu 200
601 AACGTAGACACTACAGATCCGACAGCTGACAGCGCGCGCTTCAAT 650
201 AsnValLysHisTyrLysIleArgLysLeuAspSerGlyGlyPheTyr 217
651 CACCTCCCGACACCGATTCACAGACCTGACAGACCTGCTGCTGCTGCT 700
217 eThrSerArgThrGlnPheAsnSerLeuGlnGlnLeuValAlaTyrTyr 234
701 CCAACACAGCCGATGGCTGTGCACCGCTCACACCGCTGTGCGCCAG 750
234 eLysHisAlaAspGlyLeuCysHisArgLeuThrThrValCysProThr 250
751 TCCAGCCCGACAGACTCAGGCGCTGGCCAGAGATCCTGGAGATCCCTG 800
251 SerLysProGlnThrGlnGlyLeuAlaLysAspAlaTrpGlnIlePro 267
801 GAGTGCCTCGCGCTGAGGTCAGAGCTGGCGCCAGGCGCTGTGGAGAG 850
267 gGlnSerLeuArgLeuGlnValLysLysGlnGlnGlyCysPheGlyGln 284
851 TGTGATGGGAGCTGGAACGGTACACACAGGGTGGCCATCAAAACCTG 900
284 alTrpMetGlyThrTrpAsnGlyThrThrArgValAlaIleLysThrLeu 300
901 AACCTGGACAGATGTCTCCAGAGGCTTCTCTGACAGAGCCCAAGTCA 950
301 LysProGlyThrMetSerProGlnAlaPheLeuGlnIleAlaGlnVal 317
951 GAAGAAGCTGAGAGAGAGAGAGAGCTGCTGCTGCTGCTGCTGCTGCT 1000
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1001 AGAGCCCATTTACATGCTCAGGAGTACATGAGCAGAGGAGGAGTTGCT 1050
334 lGlnProIleTyrIleValThrGlnTyrMetSerLysGlySerLeuLeu 350
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351 AspPheLeuLysGlyGlnThrGlyLysTyrLeuArgLeuProGlnLeu 367
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1151 ACTACGTCACCGGAGCTTGTGACAGCAACATCTGCTGGAGAGAAC 1200
384 snTyrValHisArgAspLeuArgAlaAlaAsnIleLeuValGlyGlnAsn 400
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401 LeuValCysLysValAlaAspPheGlyLeuAlaArgLeuIleGlnAsp 417
1251 TGAATACAGCGCGGCGAGAGTGGCAATTCCTCATCAAGTGGAGCGCT 1300
417 nGlnTyrThrAlaArgGlnGlyAlaLysPheProIleLysTrpThrAla 434
1301 CAGAAGCTGCCCTCTATGGCGGCTTACACATCAAGTGGAGAGCTGTGCT 1350
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451 PheGlyIleLeuLeuThrGlnLeuThrThrLysGlyLysArgValProTyrPr 467
1401 TGGAGTGTGAACCGCAGAGTGTCTGAGACAGGTGAGCGGGGCTACCGGA 1450
467 oGlyMetValAsnArgGlyValLysAspGlnValGlnArgGlyTyrArgm 484
1451 TGGCCTGCCCGCGAGTGTCCGAGTCCCTGACAGCATCATATGCGCAG 1500
484 eTrpCysProProGlnCysProGlnSerLeuHisAspLeuMetCysGln 500

XX 11-OCT-2001.
PD 30-MAR-2001; 2001WO-US08631.
XX 31-MAR-2000; 2000US-0540217.
XX 23-AUG-2000; 2000US-0649167.
PR (HYSE-) HYSEQ INC.
XX
XX
PI Drmanac RF, Liu C, Tang YT;
XX WPI; 2001-639362/73.
DR P-PSDB; ABG23778.
XX
XX New Isolated Polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
F responsible for genetic disorders or other traits and to assess
PA biodiversity
PS
PS Claim 1; SEQ ID NO 23769; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS6197-AAS94564 represent novel human
CC diagnostic coding sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcl_sequences.
XX
SO Sequence 1699 BP; 364 A; 532 C; 511 G; 292 T; 0 other;

Query Match 78.8%; Score 1269; DB 23; Length 1699;
Best Local Similarity 95.0%; Pred. No. 3.7e-230;
Matches 1359; Conservative 0; Mismatches 5; Indels 67; Gaps 2;

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QY 367 ctggccacactgcctcagacagagacagacagctatcccccagaacactgtgccc 426
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467 oGlyMetValAsnArgLysValLeuAspGlnValGlnArgGlyTyrArg 484
1451 TCCCTGCGCCGCGGAGTGTCCGAGTCCCTGACGACACCTCATGTGCGAC 1500
484 eTrpCysProProGlnLysProGlnSerLeuHisAspLeuMetCysGln 500
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? CITY: Fairfield
? STATE: Connecticut
? COUNTRY: USA
? ZIP: 06430
? COMPUTER READABLE FORM:
? MEDIUM TYPE: 3.5 inch, 760 Kb storage
? COMPUTER: DELL 486/50
? OPERATING SYSTEM: DOS 5.0
? SOFTWARE: Displaywrite 3
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: PCT/US93/00445
? FILING DATE: 19930105
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 07/820,011
? FILING DATE: 06-JAN-1992
? ATTORNEY/AGENT INFORMATION:
? NAME: Klee, Maurice M.
? REGISTRATION NUMBER: 30,399
? REFERENCE/DOCKET NUMBER: ALX-101PCT
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (203) 255 1400
? TELEFAX: (203) 254 1101
? INFORMATION FOR SEQ ID NO: 4:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 536 amino acids
? TYPE: AMINO ACID
? TOPOLOGY: Linear
? MOLECULE TYPE: Protein
? HYPOTHEICAL: NO
? FRAGMENT TYPE: Complete Sequence
? ORIGINAL SOURCE:
? ORGANISM: Homo sapien
? PUBLICATION INFORMATION:
? AUTHORS: Anderson, Stephen K.
? AUTHORS: Gibbs, Carol P.
? AUTHORS: Tanaka, Akio
? AUTHORS: Kung, Hsing-jien
? AUTHORS: Fujita, Donald J.
? TITLE: Human Cellular src Gene:
? TITLE: Nucleotide Sequence and Derived Amino
? TITLE: Acid Sequence of the Region Coding for
? TITLE: the Carboxy-Terminal Two-Thirds of
? JOURNAL: pp60c-src
? VOLUME: 5
? ISSUE: 5
? PAGES: 1122-1129
? DATE: May, 1985
? PUBLICATION INFORMATION:
? AUTHORS: Tanaka, Akio
? AUTHORS: Gibbs, Carol P.
? AUTHORS: Arthur, Richard R.
? AUTHORS: Anderson, Stephen K.
? AUTHORS: Kung, Hsing-jien
? AUTHORS: Fujita, Donald J.
? TITLE: DNA Sequence Encoding the
? TITLE: Amino-Terminal Region of the Human c-src
? TITLE: Protein: Implications of Sequence
? TITLE: Divergence among src-Type Kinase
? JOURNAL: Molecular and Cellular Biology
? VOLUME: 7
? ISSUE: 5
? PAGES: 1978-1983
? DATE: May, 1987
? PCT-US93-00445-4

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alignment_scores:
  quality: 2834.00      length: 536
  ratio: 5.287         gaps: 0
Percent Similarity: 100.000  Percent Identity: 100.000

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Query Match 75.5%; Score 1216.6; Db 5; Length 1602;
 Best Local Similarity 85.2%; Pred. No. 5,9e-238;
 Matches 1373; Conservative 0; Mismatches 229; Indels 9; Gaps 1.

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 DB 61 CCCGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 111
 QY 121 ccaagcctcgagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 180
 DB 112 ACAGACAG 171
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 QY 241 ccggtgacggtgagagacacacttctggtcctctatgactatgagtcagagc 300
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 QY 1321 cgttcacacatgaatgagcagcagcagcagcagcagcagcagcagcagcag 1380
 DB 1312 CGGTCACCATCAAGTGGAGTGTGCTGCTTCCGATCCTGCTGATGAGTGAAC 1371
 QY 1381 aagggagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1440
 DB 1372 AAGGGCCGGGTGCTCAATACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1431
 QY 1441 ggcacacagatccctgcagcagcagcagcagcagcagcagcagcagcagcag 1500
 DB 1432 GCGTACCGGATCCCTGCGCCGCGCAGAGTCCCGAGTCCGCTGATATAGTCCAG 1491
 QY 1501 tgcgtgcgagagagcagcagcagcagcagcagcagcagcagcagcagcagcag 1560
 DB 1492 TGCTGGCGGAG 1551
 QY 1561 gactacttcagctcagcagcagcagcagcagcagcagcagcagcagcagcag 1611
 DB 1552 GACTACTTCACCTCAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1602

RESULT 5

PCIT-US93-06251-83
 ; Sequence 83, Application PC/TUS9306251

; GENERAL INFORMATION:

; APPLICANT: Wicksstrom, Eric and Rife, Jason P.

; TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing

; TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates

; NUMBER OF SEQUENCES: 93

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER

; STREET: 400 Garden City Plaza

; CITY: Garden City

; STATE: NY

; COUNTRY: USA

; ZIP: 11530

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCIT/US93/06251

; FILING DATE: 19930630

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Digilio, Frank S.

; REGISTRATION NUMBER: 31,346

; REFERENCE/DOCKET NUMBER: 8586

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 516-742-4343

; TELEFAX: 516-742-4366

; TELEX: 230 901 SANS UR

Db 472 tccgagcggctgctgtctacaccccgaaaccccggggaaaccttctgtccgggagagc 531
 Oy 541 gagaccagaaggtgctactgctcctcagtgctgacttcgacaacgcaagggctc 600
 Db 532 gagacgacaagaagtgctcattgctcctcctcgttcttgactttgacaagcaggggctc 591
 Oy 601 aacgtgaagcactacaagatccgcaagctgagacggcggtcttctacatcacctccgc 660
 Db 592 aatgtgaagcactacaagatccgcaagctgagacggcggtcttctacatcacctccgc 651
 Oy 661 acccagttacaagcctgtagcagcgtggtgctactactccaaacgccgagtgctg 720
 Db 652 acccagttacaagcctgtagcagcgtggtgctactactccaaacgctgtagctg 711
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 Db 712 tgcacacgctcacaacgctgtagcagcgtggtgctactactccaaacgctgtagctg 771
 Oy 761 gatgcttggagagatccctcggagagctgctgagctgagagctgagagctgagagctg 840
 Db 772 gagcgttggagagatccctcggagagctgctgagctgagagctgagagctgagagctg 831
 Oy 841 ttggcggaggtgtgtagtgagagctgagagctgagagctgagagctgagagctg 900
 Db 832 ttggcggaggtgtgtagtgagagctgagagctgagagctgagagctgagagctg 891
 Oy 901 aagcctgagcagatgtctcagagagctcctcctcagagagagagagagagagagagctg 960
 Db 892 aagcctgagcagatgtctcagagagctcctcctcagagagagagagagagagagagctg 951
 Oy 961 aagcctgagcagatgtctcagagagctcctcctcagagagagagagagagagagagctg 1020
 Db 952 cggcctgagcagatgtctcagagagctcctcctcagagagagagagagagagagagctg 1011
 Oy 1021 acgagatcatatgagcaagggagaggttctgagatcttctcaaggggagagagagagagctg 1080
 Db 1012 actgagatcatatgagcaagggagaggttctgagatcttctcaaggggagagagagagagctg 1071
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 Db 1072 ctggcggcggcctcagcctggtgagatgctgctcagatcgctcagagagagagagagagctg 1131
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 Db 1132 gagcagatgagatcagctcagcagagcctggtgagagagagagagagagagagagagctg 1191
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 Db 1192 ctggtgtgcaaggtgagcagcctggtgagagagagagagagagagagagagagagagctg 1251
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 Db 1252 ggcggcgaaggtgagcagcctggtgagagagagagagagagagagagagagagagagctg 1311
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 Db 1312 cgcctcagcagatcagcagcctggtgagagagagagagagagagagagagagagagagctg 1371
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 Db 1372 aagggagcgggtgagcagcctggtgagagagagagagagagagagagagagagagagctg 1431
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 Db 1432 ggcctcagcagatcagcagcctggtgagagagagagagagagagagagagagagagagctg 1491
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RESULT 6
 AAS87964
 ID AAS87964 standard; CDNA; 1090 BP.
 XX
 AC AAS87964;
 XX
 DT 13-FEB-2002 (first entry)
 XX
 DE DNA encoding novel human diagnostic protein #23768.
 XX
 KW Human: chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.
 XX
 PR 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 DR WPI: 2001-639362/73.
 DR P-PSDB; ABG23777.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity
 XX
 PS claim 1; SEQ ID NO 23768; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AAS64197-AAS94564 represent novel human
 CC diagnostic coding sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pcl_sequences.
 XX
 SQ Sequence 1090 BP; 219 A; 331 C; 344 G; 196 T; 0 other;
 XX
 Query Match 65.7%; Score 1058; DB 23; Length 1090;
 Best Local Similarity 100.0%; Pred. No. 1.9e-190;
 Matches 1058; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 554 gtgctactgagcctcagctgctgacttgacaaagcgaagggccttaacgtgaagcact 613
 Db 1 gtgctactgagcctcagctgctgacttgacaaagcgaagggccttaacgtgaagcact 60


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QY 808 ctgcgctcgtgaggtcaagctggccagggctgtcttggcgaagtglygagtgaggacttg 867
XX |||||||
DB 454 ctgcgctcgtgaggtcaagctggccagggctgtcttggcgaagtglygagtgaggacttg 513
QY 866 aacggtacacacacaggtgtggtccatcaaaacccctgaagctggcagatgtctccagagcc 927
XX |||||||
DB 514 aacggtacacacacaggtgtggtccatcaaaacccctgaagctggcagatgtctccagagcc 573
QY 928 ttccctcgaagagccaggtcattgaagaagctgaggaagctgaggaagctggcaggtttat 987
XX |||||||
DB 574 ttccctcgaagagccaggtcattgaagaagctgaggaagctgaggaagctggcaggtttat 633
QY 988 gctgtgtgttcagagagagccattacatcgttcacaggaatcagaggaagaggtttg 1047
XX |||||||
DB 634 gctgtgtgttcagagagagccattacatcgttcacaggaatcagaggaagaggtttg 693
C 1048 ctgcgacttctcaaggggagagacaggaagctacgtgcgctgctcctaagctgtgtgacatg 1107
DB 694 ctgcgacttctcaaggggagagacaggaagctacgtgcgctgctcctaagctgtgtgacatg 753
QY 1108 gctgtcgaatcagctcgaagctggtgtcgtgtgagcgaatgagctacgtccacccggagc 1167
DB 754 gctgtcgaatcagctcgaagctggtgtcgtgtgagcgaatgagctacgtccacccggagc 813
QY 1168 ctgcgtcgaagcaacatcctgtgtgaggaagaaactgtgtgcaaaagtggcgcagcttggg 1227
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QY 1288 aagtgagcgggtccacgaagctgcctctctgtgcgcgttcacatcaagtcgaagctgttg 1347
DB 934 aagtgagcgggtccacgaagctgcctctctgtgcgcgttcacatcaagtcgaagctgttg 993
QY 1348 tccctcggagatcctgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 1407
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DB 1054 gtgaacccgagaggtgtcgtgacacaggttgagacggtgtacacgagtgctccgcgcggag 1113
QY 1468 tgtcccgagctcctcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 1527
DB 1114 tgtcccgagctcctcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 1173
QY 1528 cccacactcgaatcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 1587
DB 1174 cccacactcgaatcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 1233
QY 1588 taccagcccgaggagaaactctag 1611
DB 1234 taccagcccgaggagaaactctag 1257

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RESULT 8
AAS94859
ID AAS94859 standard; DNA: 2433 BP.

AC AAS94859;
XX
XX 14-FEB-2002 (first entry)
DE Human DNA sequence #114 expressed during foam cell differentiation.
XX
XX Human, foam cell differentiation; atherosclerosis; cerebral stroke;
KW cardiovascular disorder; coronary artery disease; gene therapy; ds.
XX
XX Homo sapiens.

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PN WO200177389-A2.
XX
XX 18-OCT-2001.
XX
XX 04-APR-2001; 2001WO-US11128.
XX
XX 05-APR-2000; 2000US-195106P.
XX
XX (INCYTE GENOMICS INC.
PA
XX Shiffman D, Somogyi R, Lawn R, Sellhammer JU, Porter GJ, Mikita T;
PI Tai J;
XX
XX WPI; 2002-010925/01.
XX
XX Composition useful for diagnosis of conditions, disorders or diseases
PT associated with atherosclerosis, comprises several polynucleotides that
PT are differentially expressed in foam cell development.
XX
XX Claim 1; Page 169; 315pp; English.
XX
XX The present invention relates to the isolation of human polynucleotide
CC sequences that are differentially expressed during foam cell
CC differentiation. The polynucleotide sequences of the invention or a
CC composition comprising these polynucleotides are useful as a high
CC throughput method for detecting altered expression of one or more
CC polynucleotides in a sample. The polynucleotides can be used in the
CC diagnosis of disorders associated with foam cell development such as
CC atherosclerosis, cerebral stroke, and cardiovascular disorders such as
CC coronary artery disease. The polynucleotide sequences can also be used
CC as PCR primers and probes. The polynucleotides of the invention are also
CC useful in gene therapy. AAS94746-AAS95021 represent the human
CC polynucleotide sequences of the invention which are differentially
CC expressed during foam cell differentiation.
XX
XX Sequence 2433 BP; 547 A; 676 C; 687 G; 523 T; 0 other;
SQ

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Query Match 50.4%; Score 811.2; DB 24; Length 2433;
Best Local Similarity 73.9%; Pred. No. 6.2e-144;
Matches 1029; Conservative 0; Mismatches 363; Indels 0; Gaps 0;

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QY 220 acctcccgcgaagggggggccgcgtggtgagtgagcttctgtgaccttctgtccctcat 279
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QY 280 gactatagctcgtgagggagacagacctgtcctcctaagaagggcgaagctccagatt 339
DB 327 gactatgaggtcgtgaactgtggtgagctcactcctcaacaaaggcgaagttccaacatc 386
QY 340 gttaacaacacgagggagacatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 399
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QY 400 taatcccccaacatcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 459
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QY 460 ggcagaatcacacgagcgggtcagagcgtttactgtcattcaatgacgaagaaccggaagg 519
DB 507 ggaagaatcgtggaagaagatgacagagagcagctgtccttcaacaggaaccggaagg 566
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DB 567 gcttctcattcgtggaagaacgagacacaaaggtgtcctcctcctcctcctcctcctgagac 626
QY 580 ttgcagaacgcgaagggcctcaacgtgaagcactacaagaatccgaaagcttgagacagggc 639
DB 627 tgggataccagccagagcgatcgtatgaagcatatacaagaatccgaaacgtgacatgggc 686
QY 640 ggtcttaatacactcccgacacccagttacaacgctgtgacagcgtgtgtgtgtgtgtgt 699
DB 687 ggtactaatacaccacacacggttcactcagtcggtgagagcgtgtgtgtgtgtgtgtgt 746

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CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 565 AA;

alignment_scores: Length: 550
 Quality: 2408.50 Gaps: 3
 Ratio: 4.946
Percent Similarity: 88.545 Percent Identity: 85.273

alignment_block:
US-09-444-711-1 x ABG23778 ..

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58  CCGCGGAGACGTGCACGCGGTGGCGGGGCGCTTCCCGGCC..... 102
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16  ProGluAlaValLeuGluSerAlaGlyAlaProAspThrProAr 32
103 .....TCGACAGCCCGCAGACGCTCGCCGAGCGGCAC 142
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32  GArGluHisSerPheThrGlnThrAlaGlySerLeuSerProGlnAlaHisA 49
143 GCGGCGCCAGCGCGCTTCGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 192
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
49  laGlyProHisThrAlaGlyLeuHisProArGlnGlnAlaHisMetAlaG 65
193 GGAGGCTTCACCTCTCGGACAC.....GTACACCTC 224
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
66  GlyGlyGlyAlaValThrAspThrAlaGlyHisIleProAsnAlaAspVa 82
225 CCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 274
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
82  lProArGlyTrpLeuThrCysThrGlyGlyValThrThrPheValAlaI 99
275 TCTAGACATATAGCTAGAGAGGAGACAGACCTGCTCTCAAGAAAGC 324
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
99  euTrpAspTrpGlySerAlaGlyThrGlnThrAspLeuSerPheGlySlyGly 115
325 GAGCGGCTCCAGATGTCTCAACAACGAGGAGGAGACTGGGTGGCGCA 374
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
116  GluAlaGlyLeuGlnIleValAlaAsnThrGlySlyAspTrpTrpLeuAlaH 132
375 CTGCGCTACAGACAGACAGACAGCTACATCCCAACAACACTACGTGGCGC 424
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
132  sSerLeuSerThrGlnThrGlnThrGlyTrpIleProSerAsnTrpValAlaI 149
425 CCTCGCATCCATCCAGGCTGAGAGGTGATTTGGCAAGATCACCAGA 474
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
149  roSerAspSerIleGlnAlaGlnGlnTrpTrpPheGlySlyIleThrAlaG 165
475 CGGAGTAGAGCGGTCTACTGCTCAATGCAGAACCGGAGGAGCGACCT 524
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
166  ArGluSerGluAlaGlyLeuLeuLeuAlaGluAsnProArGlyThrPh 182
525 CCTCTGGGAGAAAGTGAGACCAAGAGAGCTCTACTGCTCTCAAGTGT 574
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
182  eleuValAlaGlySerGluThrThrGlySlyAlaTrpCysLeuSerValS 199
575 CTGACTTGACAAAGCGCAAGGCGCTCAACGTGAAGCACTACAGATCCGC 624
   |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
199  erAspPheAspAlaGlySlyLeuAlaValGlyHisTrpTrpSlyIleAlaG 215
625 AAGCTGGACAGCGGGGCTTCTACATCACTCCGACCCAGTTCACAG 674
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216  LysLeuAspSerGlyGlyPheTrpIleThrSerArgThrGlnPheAsnSe 232
675  CTGCGACAGACTGGTGGCTACTACTCC..... 702
232  rLeuGlnGlnLeuValAlaTrpTrpSerMetSerHisCysProPheS 249
703 .....AACAC 708
249  eAlaAlaGlyTrpTrpGlyGlyGlyCysProGlnGluProGlnHis 265
709  GCCGATGCGCTGTGACCGCTCCACCGCTGACCGCTGCGCCAGCAAGCC 758
266  AlaAspGlyLeuCysHisArgLeuThrThrValCysProThrSerLysPr 282
759  GCAAGCTCAGAGGCTGGCCAAAGATGCTGGAGATCCCTCGGAGTGC 808
282  oGlnThrGlnGlyLeuAlaLysAspAlaTrpGlnIleProArGluSerL 299
809  TGGGCGCTGGAGGTCAAGCTGGCCAGGCTGCTTGGCGAGGTGTGATG 858
299  euArGlyLeuGluValLysLeuGlyGlnGlyCysPheGlyGlyValTrpMet 315
859  GGGACCTGGAACGGTACCACAGGCTGGCCATCAAAACCTGAAGCTCG 908
316  GlyThrTrpAsnGlyTrpThrArgValAlaIleLysThrLeuLysProGl 332
909  CAGCATGTCTCCAGAGGCTTCTCTGACAGAGCGCCAGCTCATGAAGAAGC 958
332  yTrpMetSerProGlnAlaPheLeuGlnGlnAlaGlnValMetLysLysL 349
959  TGAAGCATGAAGACTGGTGCAGTTGTATGCTGTGTTTCAGAGAGGCC 1008
349  euArGlnGlyLysLeuValGlnLeuTrpAlaValAlaSerGlnGluPro 365
1009  ATTACATGCTCAGGAGTACATGAGCAGAGGAGTGTGCTGAGCTTCT 1058
366  lIleTrpIleValThrGlyTrpMetSerLysGlySerLeuLeuAspPheLe 382
1059  CAAAGGGGAGACAGAGCAAGTACCTGCGGCTGCTCAGCTGGTGGACATGG 1108
382  uLysGlyGlnThrGlyLysTrpLeuArGlyLeuProGlnLeuValAspMetA 399
1109  CTGCTCAGATCGCTCAGGCAATGCGGTACGTGAGCGGATGAACTACGTC 1158
399  laAlaGlnIleAlaSerGlyMetAlaTrpAlaGluArgMetAsnTrpVal 415
1159  CACGGGACCTGCTGACGACCAACATCTGCTGGGAGAGAACCTGGTGTG 1208
416  HisArgAspLeuArGlnAlaAlaAsnIleLeuValGlyGluAsnLeuValCy 432
1209  CAAAGTGGCGGACTTGGGCTGCTCGCTCATTTGAAGACATAGTACA 1258
432  sLysValAlaAspPheGlyLeuAlaArgLeuIleGluAspAsnGluTrpTr 449
1259  CGGCGCGGCAAGGTGCCAAATTCCTCCATCAAGTGGAGCGGCTCCAGAACT 1308
449  hrAlaArgGlnGlyAlaLysPheProIleLysTrpThrAlaProGluAla 465
1309  GCGCTCATGCGCGCTTCAACATCAAGTGGAGCTGAGTCTCGGAGAT 1358
466  AlaLeuTrpGlyArgPheThrIleLysSerAspAlaTrpSerPheGlyTr 482
1359  CTTGCTAGCTGAGCTCACCAAGAGGAGCGGCTTACCTCGGAGTGG 1408
482  eleuLeuThrGluLeuThrThrLysGlyAlaGlyAlaProTrpProGlyMetV 499
1409  TGAACCGGAGGTGTGGACAGGTGAGCGGCGGCTACCGGATGCCCTGC 1458
499  AlaAsnArgGluValLeuAspGlnValGluArgGlyTrpArgMetProCys 515
1459  CCGCGGAGTGTCCGAGTCCCTGACAGACCTCATGTGCCAGTGTCTGGC 1508
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 Db 716 gattcatttgaatccctggaataacagaggtatttcttagtaagaagatgaaacaa 775
 Oy 548 cgaaggtgacctgacctcagtgctgacttcgacacagccagggccctcaacgtga 607
 Db 776 ctaaggtgctattcccttcttctatcgtgattggaatgagaaaggtgtaacagtga 835
 Oy 608 agcactacaagaatccgcaagctggaagcggcgtcttacaacctcccgcaaccagt 667
 Db 836 aacctacaagaatggaacctggaacatggtgatactatatacacaacagagcaaat 895
 Oy 668 tcaaacgctgacagcagcgtggtgactactacacaaacgcgcgtgctgctgcaac 727
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 Db 1016 gggaaatccctcgagaatcttgcgactagaggttaactagacagagatgttcgcgc 1075
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 ID AAH28359 standard; cDNA; 4517 BP.
 XX
 AC AAH28359;
 XX
 DT 05-SEP-2001 (first entry)
 XX
 DE Nucleotide sequence of human tyrosine kinase protein Yes.
 XX
 KW Vascular permeability; tyrosine kinase protein; Src; Yes; stroke;
 KW myocardial infarction; restenosis; trauma; blood vessel; atherosclerosis;
 KW diabetic retinopathy; inflammatory disease; infection; arthritis;
 KW adult respiratory distress syndrome; ARDS; rheumatoid arthritis;
 KW diabetic retinopathy; psoriasis; neovascular glaucoma;
 KW capillary proliferation; osteoporosis; cancer; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FT CDS Location/Qualifiers
 FT 208..1839
 FT /*tag- a
 FT /*product= "Yes"
 XX
 PN WO200145751-A1.
 XX
 PD 28-JUN-2001.
 XX
 PF 22-DEC-2000; 2000MO-US35396.
 XX
 PR 22-DEC-1999; 9905-0470881.
 PR 29-MAR-2000; 2000US-0538248.
 XX
 PA (SCRI) SCRIPPS RES INST.
 XX
 PI Cheresah DA, Elliceir B, Paul R;
 XX
 DR WPI; 2001-417982/44.
 DR P-PSDB; AAB84663.
 XX
 PT Modulating vascular permeability in tissues, including inflamed tissue,
 PT tissues associated with stroke, myocardial infarction, by contacting
 PT the tissue with tyrosine kinase protein Src, Yes or their modified
 PT forms
 XX
 PS Disclosure; Fig 12; 133pp; English.
 XX
 CC The specification describes a method for modulating vascular
 CC permeability in a tissue suffering from a disease condition. The method
 CC comprises contacting the tissue with a pharmaceutical composition
 CC comprising tyrosine kinase protein Src, Yes or their mixtures or
 CC nucleic acid expressing them. The method is useful for modulating
 CC vascular permeability in tissues, including inflamed tissue, tissues
 CC associated with stroke, myocardial infarction or other blockage of
 CC normal flow, tissues undergoing restenosis, psoriatic, renal tissue
 CC and similar tissues. Pathologies which may be treated include such as
 CC trauma to blood vessels, and other systemic pathological events such as
 CC atherosclerosis, diabetic retinopathy, inflammatory disease due to
 CC infection by microbial agents and arthritis. Other diseases which can
 CC be treated include adult respiratory distress syndrome (ARDS), rheumatoid
 CC arthritis, diabetic retinopathy, psoriasis, neovascular glaucoma,
 CC capillary proliferation in atherosclerotic plaques and osteoporosis and
 CC cancer associated disorders such as solid tumours, solid tumour
 CC metastases, angiofibromas and hemangiomas. The present sequence
 CC encodes human Yes, and is used in the method of the invention.
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298 GlyThrThrLysValAlaIleLysThrLeuLysProGlyThrMetMetPr 314
921 AGAGGCTTCCTGAGAGGCGCCAGTCATGAAAGCTAGCATGAGTAGA 970
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331 yLeuValAlaProLeuThrAlaValAlaValSerGlnLysProIleThrIleVal 347
1021 AGGAGTACATGAGCAAGGGGAGTGTCTGAGACTTCTCAAGGGGAGAC 1070
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1371 GGTCAACACAAAGGAGCGGCTGCGCTACCCCTGGAGTGTGAACCGGAGG 1420
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498 ProGlnSerLeuHisGlnLeuMetAsnLeuGlyStrpLysLysAspProAs 514
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514 pGlnArgProThrPheGlnThrGlyIleGlnSerPheLeuGlnAspThrPhe 531
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ID AAB84663 standard; Protein; 543 AA.
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AC AAB84663;
XX
DT 05-SEP-2001 (first entry)
XX
DE Amino acid sequence of human tyrosine kinase protein yes.
XX
KW Vascular permeability; tyrosine kinase protein; Src; Yes; stroke;
KW myocardial infarction; restenosis; trauma; blood vessel; atherosclerosis;
KW diabetic retinopathy; inflammatory disease; infection; arthritis;
KW adult respiratory distress syndrome; ARDS; rheumatoid arthritis;
KW diabetic retinopathy; psoriasis; neovascular glaucoma;
KW capillary proliferation; osteoporosis; cancer.
XX
OS Homo sapiens.
XX
PN MO200145751-A1.
XX
PD 28-JUN-2001.
XX
PF 22-DEC-2000; 2000MO-US35396.
XX
PR 22-DEC-1999; 99US-0470881.
PR 29-MAR-2000; 2000US-0538248.
XX
PA (SCRI) SCRIPPS RES INST.
XX
PI Cheresh DA, Ellicelri B, Paul R;
XX
DR WPI: 2001-417982/44.
XX
DR N-PSDB; AAH28359.
XX
PT Modulating vascular permeability in tissues, including inflamed tissue,
PT tissues associated with stroke, myocardial infarction, by contacting
PT the tissue with tyrosine kinase protein Src, Yes or their modified
PT forms
XX
PS Disclosure; Fig 11; 133pp; English.
XX
PS
XX
CC The specification describes a method for modulating vascular
CC permeability in a tissue suffering from a disease condition. The method
CC comprises contacting the tissue with a pharmaceutical composition
CC comprising tyrosine kinase protein Src, Yes or their mixtures or
CC nucleic acid expressing them. The method is useful for modulating
CC vascular permeability in tissues, including inflamed tissue, tissues
CC associated with stroke, myocardial infarction or other blockage of
CC normal flow, tissues undergoing restenosis, psoriatic, retinal tissue
CC and similar tissues. Pathologies which may be treated include trauma
CC trauma to blood vessels, and other systemic pathological events such as
CC atherosclerosis, diabetic retinopathy, inflammatory disease due to
CC infection by microbial agents and arthritis. Other diseases which can
CC be treated include adult respiratory distress syndrome (ARDS), rheumatoid
CC arthritis, diabetic retinopathy, psoriasis, neovascular glaucoma,
CC capillary proliferation in atherosclerotic plaques and osteoporosis and
CC cancer associated disorders such as solid tumours, solid tumour
CC metastases, angiofibromas and hemangiomas. The present sequence
CC represents human Yes, and is used in the method of the invention.
XX
SO Sequence 543 AA:

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Ratio:	4.480	Gaps:	4
Percent Similarity:	86.813	Percent Identity:	74.542

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Align seg 1/1 to: AAB84663 from: 1 to: 543
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CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (ii) and its binding partners are useful in medical
 CC imaging of sites expressing (ii). (i) and (ii) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. AA664197-AA694564 represent novel human
 CC diagnostic coding sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pcl_sequences.
 CC XX
 CC Sequence 4517 BP; 1437 A; 784 C; 955 G; 1341 T; 0 other;

Very Match 44.1%; Score 710.2; DB 23; Length 4517;
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 matches 955; Conservative 0; Mismatches 408; Indels 0; Gaps 0;

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DT 13-MAR-2000 (first entry)

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DE Protein kinase A; PKA; PKA signaling pathway; phosphorylation; cancer;

KW kinase substrate; immunosuppressive disorder; proliferative disease;

KW HIV infection; AIDS; immunodeficiency; autoimmune disease;

OS systemic lupus erythematosus; Src-family; ss.

XX Homo sapiens.

XX MO962315-A2.

XX 02-DEC-1999.

XX 27-MAY-1999; 99WO-GB01680.

XX 27-MAY-1998; 98NO-0002419.

XX 30-DEC-1998; 98DS-0114240.

XX (LAUR-) LAURAS AS.

XX (JONE/) JONES E L.

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XX

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XX

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CC associated and over expressed proto-oncogenes.

Sequence 1804 BP; 595 A; 331 C; 428 G; 450 T; 0 other;

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Job time: 4213 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 4, 2002, 08:26:28 ; Search time 54.19 Seconds
(Without alignments)
7302.373 Million cell updates/sec.

Title: US-09-444-711-1

Perfect score: 1611
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Se-arched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1609.4	99.9	1611	1 US-07-820-011A-3	Sequence 3, Appl
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3	1216.6	75.5	1602	1 US-07-820-011A-1	Sequence 1, Appl
4	1216.6	75.5	1602	5 PCT-US93-00445-1	Sequence 1, Appl
5	710.2	44.1	4517	5 PCT-US93-06251-83	Sequence 83, Appl
6	689.4	42.8	2647	5 PCT-US93-06251-77	Sequence 77, Appl
7	539.8	33.5	1804	1 US-08-306-691B-40	Sequence 40, Appl
8	539.8	33.5	1804	5 PCT-US93-06251-82	Sequence 82, Appl
9	465.8	28.9	1491	2 US-09-006-675-1	Sequence 1, Appl
10	465.8	28.9	1491	4 US-09-228-603A-1	Sequence 1, Appl
11	346.2	21.5	1574	3 US-09-173-581-12	Sequence 12, Appl
12	346.2	21.5	1574	4 US-09-420-915-12	Sequence 12, Appl
13	341.6	21.2	780	4 US-09-006-675-7	Sequence 7, Appl
14	341.6	21.2	780	4 US-09-228-603A-7	Sequence 7, Appl
15	284	17.6	2770	4 US-08-426-509A-5	Sequence 5, Appl
16	284	17.6	2770	5 PCT-US95-05008-5	Sequence 5, Appl
17	284	17.6	7607	1 US-08-426-509A-5	Sequence 5, Appl
18	252	15.6	271	1 US-08-306-691B-19	Sequence 19, Appl
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20	252	15.6	271	5 PCT-US93-06251-66	Sequence 24, Appl
21	249.6	15.5	3623	1 US-08-306-691B-35	Sequence 66, Appl
22	217.6	13.5	728	4 US-09-328-111-821	Sequence 82, Appl
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24	212.4	13.2	1398	2 US-08-604-989A-10	Sequence 10, Appl
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28	210.8	13.1	255	1 US-08-306-691B-34	Sequence 34, Appl
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33	203.4	12.6	2574	4 US-09-142-529-2	Sequence 2, Appl
34	200	12.4	1987	2 US-08-876-882-1	Sequence 1, Appl
35	182	11.3	194	1 US-08-306-691B-30	Sequence 30, Appl
36	182	11.3	194	5 PCT-US93-06251-72	Sequence 72, Appl
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39	165	10.2	3546	1 US-08-162-809-13	Sequence 9, Appl
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45	161	10.0	4097	1 US-08-162-809-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-07-820-011A-3
Sequence 3, Application US/07820011A
Patent No. 5336615
GENERAL INFORMATION:
APPLICANT: Bell, Leonard
APPLICANT: Madi, Joseph A.
APPLICANT: Warren, Stephen L.
APPLICANT: Luthinger, Daniel J.
TITLE OF INVENTION: Genetically Engineered
TITLE OF INVENTION: Endothelial Cells Exhibiting Enhanced
TITLE OF INVENTION: Migration
TITLE OF INVENTION: and Plasmidogen Activator Activity
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Maurice M. Klee
STREET: 1951 Burr Street
CITY: Fairfield
STATE: Connecticut
COUNTRY: USA
ZIP: 06430
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb storage
COMPUTER: IBM PC XT
OPERATING SYSTEM: PC-DOS/MS-DOS 2.10
SOFTWARE: Displaywrite 3
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/820, 011A
FILING DATE: 19920106
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Klee, Maurice M.
REGISTRATION NUMBER: 30,399
REFERENCE/DOCKET NUMBER: 1B-101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 255 1400
TELEFAX: (203) 254 1101
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1611
TYPE: NUCLEIC ACID
STRANDEDNESS: Double
TOPOLOGY: Linear
MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapien
POSITION IN GENOME:
CHROMOSOME/SEGMENT: Chromosome 20

DB 1561 GACTACTTCAGTCCACCGAGCCCACTACCGAGCCCGGAGAACCTCTAG 1611

RESULT 2

PCT-US93-00445-3

Sequence 3, Application PC/TUS9300445

GENERAL INFORMATION:

APPLICANT: Bell, Leonard

APPLICANT: Madril, Joseph A.

APPLICANT: Warren, Stephen L.

APPLICANT: Luthringer, Daniel J.

TITLE OF INVENTION: Genetically Engineered

TITLE OF INVENTION: Endothelial Cells

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Maurice M. Klee

STREET: 1951 Burr Street

CITY: Fairfield

STATE: Connecticut

COUNTRY: USA

ZIP: 06430

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 760 kb storage

COMPUTER: DELL 486/50

OPERATING SYSTEM: DOS 5.0

SOFTWARE: Displaywrite 3

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/00445

FILING DATE: 19930105

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/820,011

FILING DATE: 06-JAN-1992

ATTORNEY/AGENT INFORMATION:

NAME: Klee, Maurice M.

REGISTRATION NUMBER: 30,399

REFERENCE/DOCKET NUMBER: ALX-101PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: (203) 255 1400

TELEFAX: (203) 254 1101

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 1611

TYPE: NUCLEIC ACID

STRANDEDNESS: Double

TOPOLOGY: Linear

MOLECULE TYPE: cDNA to mRNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Homo sapien

POSITION IN GENOME:

CHROMOSOME/SEGMENT: Chromosome 20

PUBLICATION INFORMATION:

AUTHORS: Anderson, Stephen K.

AUTHORS: Gibbs, Carol P.

AUTHORS: Tanaka, Akio

AUTHORS: Kung, Hsing-Jien

AUTHORS: Fujita, Donald J.

TITLE: Human Cellular src Gene:

TITLE: Nucleotide Sequence and Derived Amino

TITLE: Acid Sequence of the Region Coding for

TITLE: the Carboxy-Terminal Two-Thirds of

TITLE: pp60c-src

JOURNAL: Molecular and Cellular Biology

VOLUME: 5

ISSUE: 5

PAGES: 1122-1129

DATE: May, 1985

PUBLICATION INFORMATION:

AUTHORS: Tanaka, Akio

AUTHORS: Gibbs, Carol P.

AUTHORS: Arthur, Richard R.

AUTHORS: Anderson, Stephen K.

AUTHORS: Kung, Hsing-Jien

AUTHORS: Fujita, Donald J.

TITLE: DNA Sequence Encoding the

TITLE: Amino-Terminal Region of the Human c-src

TITLE: Protein: Implications of Sequence

TITLE: Divergence among src-Type Kinase

TITLE: Oncogenes

JOURNAL: Molecular and Cellular Biology

VOLUME: 7

ISSUE: 5

PAGES: 1978-1983

DATE: May, 1987

PCT-US93-00445-3

Query Match 99.9%; Score 1609.4; DB 5; Length 1611;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1610; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB	61	GCCGAGAACGTCACAGCGGCTGAGCGGGGCGCTTCCCGCTCCAGACCCCAAGCAAG	120
QY	121	ccagcctcgccgcagagcgccagcgagcccgagcgcttgcggcgccgagcgag	180
DB	121	CCAGCCTCGCCGCGAGCGGCGGCGCCCGAGCGGCGCTTGCCTCCGCGCGCGGAG	180
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DB	181	CCCAAGCTGTTCCGAGGCTTCAACTCTCGACACGCTACCTCCCGGAGAGGGGCGG	240
QY	241	ccgctgagcggttgagtgacacacttgctgacctatgactatgagtcagagcagag	300
DB	241	CCGCTGAGCGGTGAGTGACACACTTGTGCTCTATGACTATGAGTCTAGAGGAG	300
QY	301	acagacctgtcctcacaagaagcgagcgctccagatgttcaacaacacgagagagc	360
DB	301	ACAGACCTGTCTCTCAAGAAAGCGAGCGGCTCCAGATTGTCAACAACACAGAGGAGAC	360
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QY	481	tcaagagcggttacgctcaatgacagagacccgagagagacccctcgtgagaaagt	540
DB	481	TCAAGAGCGGTACGCTCAATGACAGAGACCCGAGAGGAGACCTCTCTGAGAGAAAT	540
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QY	661	accagcttcaacagcctgacagagctggtgacctactccaacaacgagcgatggcgtg	720
DB	661	ACCCAGTTCACACAGCTGACAGAGCTGCTGCTACTCTCCAAACAGCCCATGGCTG	720
QY	721	tgcacacgctccacacacgctgtgcccacgctcacaagcgagagcagggctgccaag	780
DB	721	TGCACACGCTCCACACCGCTGTGCCACGCTCAAGCGGCAACTCAAGGCTGCGCAAG	780
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INFORMATION FOR SEQ ID NO: 83:

SEQUENCE CHARACTERISTICS:
 LENGTH: 4517 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 PCT-0593-06251-83

Query Match 44.1%; Score 710.2; DB 5; Length 4517;
 Best Local Similarity 70.1%; Pred. No. 2,2e-135;
 Matches 955; Conservative 0; Mismatches 408; Indels 0; Gaps 0;

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 Db 536 TTTCAATTAGAAAGGCTGAAGATTCATTAATTAACATACGAGAGGAGATTGGGG 595
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 Db 1316 TTCCACAGCTGTTGATATGAGCTGCTCAGATTCCTGATGATGATATTTGAAGAA 1375

Qy 1148 tgaactacaccgagactcgtgagccaacatccctgtggtgagagacctgtgt 1207
 Db 1376 TGAATATATTCACCGAGATCTTGGCGCTGCTAATATCTTGTAGAGAAATCTTGTGT 1435
 Qy 1208 gcaagtgccgacttggctgtgctgcgtcactatgaacaatgagacagcgcg 1267
 Db 1436 GCAAAATAGCAGACTTGTGTAGCAAGGTTAATTAAGACAAATGATACAGCAGAGAC 1495
 Qy 1268 aagtgccaatttcccatcaagtgtgagcgtccagaagctgcctcatatgcccctta 1327
 Db 1496 AAGGTGCAAAATTTCCATCAAAATGAGACGCTCCGAAAGCTGCACTGATGTCGTTTA 1555
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 Db 1556 CAATTAAGTGTGATGTGCTGCTATTTGGAATTCGAACAGAACTACTATCAAAAGGGCC 1615
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 Db 1616 GAGTGCCATATTCAGAGTATGTTGAACCGTGAAGTACTGAAACAAATGAGAGGATACA 1675
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RESULT 6
 PCT-US93-06251-77
 Sequence 77: Application PC/TUS9306251
 GENERAL INFORMATION:
 APPLICANT: Wickstrom, Eric and Rife, Jason P.
 TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing
 TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates
 NUMBER OF SEQUENCES: 93
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
 STREET: 400 Garden City Plaza
 CITY: Garden City
 STATE: NY
 COUNTRY: USA
 ZIP: 11530
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US93/06251
 FILING DATE: 19930630
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Disigilio, Frank S.
 REGISTRATION NUMBER: 31,346
 REFERENCE/DOCKET NUMBER: 8586
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 516-742-4343
 TELEFAX: 516-742-4366
 TELEX: 230 901 SANS UR
 INFORMATION FOR SEQ ID NO: 77:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2647 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)

QY 924 ggccttcctcagagagccagatcatalgaadagctgagcatagaaqctggtcatt 983
 Db 807 TGCCTTCCTTGAAGAGCAATCTGATGAGAGAGCTGCAGCATGACCGCTGTCGGTT 866
 QY 984 gtagc---gtgtttcagagagccatttaactcgtcagagatcagagagag 1040
 Db 867 GCATGCGGTTGTGACTAGGGGAGCAATATATATATCTGATGATGCAAAAGG 926
 QY 1041 gaattgctgacttctcaaggagagagagagagagagagagagagagagagagag 1100
 Db 927 CAGTTTCTGATTTCTCTGAAAATGAAAGAGATAGCAGCACTCTGATTCATCTAT 986
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 RESULT 10
 US-09-228-603A-1
 Sequence 1, Application US/09228603A
 Patent No. 6291651
 GENERAL INFORMATION:
 APPLICANT: Hemmati-Briyanlou, Ali
 TITLE OF INVENTION: A NOVEL SRC-FAMILY KINASE AND METHODS OF
 TITLE OF INVENTION: USE THEREOF
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Klaunder & Jackson
 STREET: 411 Hackensack Avenue, 4th Floor
 CITY: Hackensack
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07601
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/228,603A

FILING DATE: 12-JAN-1999
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Jackson Esq., David A.
 REGISTRATION NUMBER: 26,742
 REFERENCE/DOCKET NUMBER: 600-1-217 N
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-487-5800
 TELEFAX: 201-343-1684
 TELEX: 133521
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1491 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHEetical: NO
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..1491
 US-09-228-603A-1
 Query Match 28.9% Score 465.8 DB 4; Length 1491;
 Best Local Similarity 61.6% Pred. No. 5.2e-86;
 Matches 822; Conservative 0; Mismatches 492; Indels 21; Gaps 4;
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Date: Jun 4, 2002 10:37 AM

About: Results were produced by the Gencore software, version 4.5,
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Search information block:

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Query length: 1611
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Search time (sec): 33.960000

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  Patent No. 5336515
  GENERAL INFORMATION:
  APPLICANT: Bell, Leonard
  APPLICANT: Madril, Joseph A.
  APPLICANT: Warren, Stephen L.
  APPLICANT: Lutheringer, Daniel J.
  TITLE OF INVENTION: Genetically Engineered
  TITLE OF INVENTION: Endothelial Cells Exhibiting Enhanced
  TITLE OF INVENTION: Migration
  TITLE OF INVENTION: and Plasminogen Activator Activity
  NUMBER OF SEQUENCES: 4
  CORRESPONDENCE ADDRESS:
  ADDRESSEE: Maurice M. Klee
  STREET: 1951 Burr Street
  CITY: Fairfield
  STATE: Connecticut
  COUNTRY: USA
  ZIP: 06430
  COMPUTER READABLE FORM:
  MEDIUM TYPE: 5.25 inch, 360 kb storage
  COMPUTER: IBM PC XT
  OPERATING SYSTEM: PC-DOS/MS-DOS 2.10
  SOFTWARE: Displaywrite 3
  CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/07/820,011A
  FILING DATE: 19920106
  CLASSIFICATION: 435
  ATTORNEY/AGENT INFORMATION:
  NAME: Klee, Maurice M.
  REGISTRATION NUMBER: 30,399
  REFERENCE/DOCKET NUMBER: LB-101
  TELECOMMUNICATION INFORMATION:
  TELEPHONE: (203) 255 1400
  TELEFAX: (203) 254 1101
  INFORMATION FOR SEQ ID NO: 4:
  LENGTH: 536 amino acids
  TYPE: AMINO ACID
  TOPOLOGY: Linear
  MOLECULE TYPE: Protein
  HYPOTHEetical: NO
  FRAGMENT TYPE: Complete Sequence
  ORIGINAL SOURCE:
  ORGANISM: Homo sapien
  PUBLICATION INFORMATION:
  AUTHORS: Anderson, Stephen K.
  AUTHORS: Gibbs, Carol P.
  AUTHORS: Tanaka, Akio
  AUTHORS: Kung, Hsing-jien
  AUTHORS: Fujita, Donald J.
  TITLE: Human Cellular src Gene:
  TITLE: Nucleotide Sequence and Derived Amino
  TITLE: Acid Sequence of the Region Coding for
  TITLE: the Carboxy-Terminal Two-thirds of
  JOURNAL: pp60c-src
  VOLUME: 5
  ISSUE: 5
  PAGES: 1122-1129
  DATE: May, 1985
  PUBLICATION INFORMATION:
  AUTHORS: Tanaka, Akio
  AUTHORS: Gibbs, Carol P.
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ent No. 6326469

GENERAL INFORMATION:

APPLICANT: Ullrich, Axel

APPLICANT: Gshlitzky, Mikhail

APPLICANT: Sures, Irman G.

TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESS: Pennie & Edmonds

CITY: New York,

STATE: NY

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/426,509A

FILING DATE: 21-APR-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/232,545

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7683-0074-999

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-790-9090

TELEFAX: 212-869-9741

TELEX: 66141 PENNTE

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; GENERAL INFORMATION:
; APPLICANT: Sugen, Inc.
; APPLICANT: 515 Galveston Drive
; APPLICANT: Redwood City, California 94063-4720

ORIGINAL SOURCE:
ORGANISM: Gallus, gallus
PUBLICATION INFORMATION:
AUTHORS: Takeya, Tatsuo
TITLES: Hanafusa, Hidesaburo
TITLE: Structure and Sequence of the
TITLE: Cellular Gene Homologous to the RSV src
TITLE: Gene and the Mechanism for Generating the
TITLE: Transforming Virus
JOURNAL: Cell
VOLUME: 32
PAGES: 881-890
DATE: March, 1983
PCT-US93-00445-2

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: Sequence 14. Application PC/TUS9505008
: GENERAL INFORMATION:
: APPLICANT: Sugen, Inc.
: APPLICANT: 515 Galveston Drive
: APPLICANT: Redwood City, California 94063-4720
: APPLICANT: United States of America
: APPLICANT: Missenschaften E.V.
: APPLICANT: Hofgarten Str. 2
: APPLICANT: Munchen 80539
: APPLICANT: Germany
: TITLE OF INVENTION: Novel Megakaryocytic Protein Tyrosine
: TITLE OF INVENTION: Kinases
: NUMBER OF SEQUENCES: 21

```

```

: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Penile & Edmonds
: STREET: 1155 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 10036
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US95/05008
: FILING DATE: 24-APR-1995
: CLASSIFICATION:
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: US 08/232,545
: FILING DATE: 22-APR-1994
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Coruzel, Laura A.
: REGISTRATION NUMBER: 30,742
: REFERENCE/DOCKET NUMBER: 7683-074
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212)790-9090
: TELEFAX: (212)869-9741
: TELEX: 66141 PENNIE
: INFORMATION FOR SEQ ID NO: 14:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 543 amino acids
: TYPE: amino acid
: STRANDEDNESS: unknown
: TOPOLOGY: unknown
: MOLECULE TYPE: protein
: PCT-US95-05008-14

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alignment_scores:
  Quality: 2123.50      Length: 546
  Ratio: 4.480          Gaps: 4
  Percent Similarity: 86.813  Percent Identity: 74.542

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alignment_block:

US-09-444-711-1 x PCT-US95-05008-14 ..

Align seq 1/1 to: PCT-US95-05008-14 from: 1 to: 543

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1 ATGGGTAGCAACAGAGCAAGCCC..AAGATGCCAGCAGCGCGCG 47
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1 MetGlyCysIleLysSerLysGlnAsnLysSerProAlaIleLysTyrAlr 17
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48 CAGCGTGGAGCCCGCCGAGACGTGCAGCGGCGGCGGCGG.....GGCG 91
|||||
17 pProGlnAsnThrProGlnProValSerThrSerValSerHisTyrGlyAlr 34
|||||
34 LagluProThrThrValSerProCysProSerSerSerAla..... 47
|||||
142 CGCGGCGCCAGCGCGGCTTGGCCCCCGCGCGCGCGAGCCC..... 183
|||||
48 LysGlyThrAlaValAsnPheSerSerLeuSerMetThrProPheGlyG 64
|||||
184 .....AAGCTGTGCGAGGCTTCAACTCCCGGACAGCCGCA 220
|||||
64 ySerSerGlyValThrProPheGlyGlyAlaSerSerSerPheSerVal 81
|||||
221 CTTCCCGCAGAGAGGCGCGCGCTGCGCGGCTGAGTACCACTTTGTTG 270
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81 alProSerSerTyrProAlaGlyLeuThrGlyGlyValThrIlePheVal 97
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271 GCCCTGATGACTATGAGTCTAGACGAGAGACAGACTGCTCTTCAAGA 320

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/ INFORMATION FOR SEQ ID NO: 12:

/ SEQUENCE CHARACTERISTICS:

/ LENGTH: 536 amino acids

/ TYPE: amino acid

/ STRANDEDNESS: unknown

/ TOPOLOGY: unknown

/ MOLECULE TYPE: NO. 6326469e

US-08-426-509A-12

alignment_scores:

Quality: 1949.00

Ratio: 4.350

Percent Similarity: 84.848 Percent Identity: 71.023

alignment_block:

us-09-444-711-1 x US-08-426-509A-12

from 1/1 to: US-08-426-509A-12 from: 1 to: 536

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8 GlutylserGlyGlyGlnGlySerGlyThrGlyThrProAl 24
   |||:|||||:|||||:|||||:|||||:|||||:
93 TTTCCCGCGCTCGAGACCCCGACAGCCCTCGCCGACGCG... 138
   |||:|||||:|||||:|||||:|||||:|||||:
24 AHisProSerGlnTyraSPProAspProThrGlnLeuSerGlyAlaP 41
   |||:|||||:|||||:|||||:|||||:|||||:
139 .....CACCGGGGCCCCGCGCGCTCGCCCGCGCGCGCGACGCC 183
   |||:|||||:|||||:|||||:|||||:|||||:
41 heThrHisIleProAspPheAsnAsnPheHisAlaAlaValSerPro 57
   |||:|||||:|||||:|||||:|||||:|||||:
184 AAGCTG...TTCCGAGGCTTCACACTCTCGGACACCTGACCTCCCGCA 230
   |||:|||||:|||||:|||||:|||||:|||||:
58 ProValProPheSerGlyProGlyPheTyProCysAsnThrLeuGlnAl 74
   |||:|||||:|||||:|||||:|||||:|||||:
231 GAGGGCGGGCGCGCTGGCGGTGAGTACACCTTTGTGGCGCTGTATG 280
   |||:|||||:|||||:|||||:|||||:|||||:
74 AHisSerSerIleThrGlyGlyValThrLeuPheIleAlaLeuTyra 91
   |||:|||||:|||||:|||||:|||||:|||||:
281 ACPTAGAGTTCAGGACGAGACAGACCTGTCTTCAGAAAGGCGGAGG 330
   |||:|||||:|||||:|||||:|||||:|||||:
91 sPlyrGlnAlaArgThrGlnAspAspLeuSerPheGlnLysGlyLys 107
   |||:|||||:|||||:|||||:|||||:|||||:
331 CTCAGATTGTCAACAACACGAGGAGACTGTGGTGGCCACTGCT 380
   |||:|||||:|||||:|||||:|||||:|||||:
108 PheHisIleIleAsnAsnThrGlnGlyAspTrpTrpGlnAlaArgSerIle 124
   |||:|||||:|||||:|||||:|||||:|||||:
381 CAGCAGACGAGACAGAGGCTACATCCCGACACTAGTGGCGCGCTCG 430
   |||:|||||:|||||:|||||:|||||:|||||:
124 uSerSerGlyAlaThrGlyTyIleProSerAsnTyValAlaProValA 141
   |||:|||||:|||||:|||||:|||||:|||||:
431 ACCTCAGCCAGGCTGAGGAGTGATTTGGCAAGATACACGAGGAGAG 480
   |||:|||||:|||||:|||||:|||||:|||||:
141 sPserIleGlnAlaGlnGlnTrpTrpThrPheGlyLysIleGlyAlaArgLysAsp 157
   |||:|||||:|||||:|||||:|||||:|||||:
481 TCAGAGCGGTTACTGTCTCAATGTCAGAGAACCCGAGAGGAGACTTCTGT 530
   |||:|||||:|||||:|||||:|||||:|||||:
158 AlaeGlnArgGlnLeuLeuCysHisGlyAsnGlySarGlyThrPheLeuI 174
   |||:|||||:|||||:|||||:|||||:|||||:
531 GCGAGAAAGTGAGACACGAAAGGTGCTACTGCTCTCAGTGTGTGAT 580
   |||:|||||:|||||:|||||:|||||:|||||:
174 eaArgGlnSerGlnThrThrLysGlyAlaTyrserLeuSerIleArgAspTr 191
   |||:|||||:|||||:|||||:|||||:|||||:
581 TCAGCAACGCCAAGGCGCTCAACTGAAAGCACTACAAATCCGACAGTG 630
   |||:|||||:|||||:|||||:|||||:|||||:
191 rPaspGlnAlaLysGlyAspHisValLysHisTyLysIleArgLysLeu 207
   |||:|||||:|||||:|||||:|||||:|||||:
631 GACAGCGGCGGCTTCTACATCACTCCCGACCCGATTCACAGAGCTTGA 680
   |||:|||||:|||||:|||||:|||||:|||||:
208 AspSerGlyGlyTyTrIleThrThrArgAlaGlnPheAspThrIleGln 224
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681 GCACTGTGTGCTTACTACTCAACAACGCGGATGCGCTGTGCCACCGCC 730

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224 nGlnLeuValGlnHisTyTrIleGlnArgAlaAlaGlyLeuCysCysArgL 241
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731 TCACACCGCTGTGCCCCACGTCACAGCCCGACACTAGAGGCGCTGGCC... 777
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
241 euAlaValProCysProLysGlyThrProLysLeuAlaAspLeuSerVal 257
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
778 .....AAGATGCTCTGGAGATCCCTCGGGAGTCCGCTGGCGCTGAGGT 821
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
258 LysThrLysAspValTrpGlnIleProArgGlnSerLeuGlnLeuGln 274
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822 CAAGTGGGCGCAGGGCGCTTGGCGAGGTGTGAGTGGAGGAGACTGGAGAC 871
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
274 nLysLeuGlyAsnGlyGlnPheGlyGlnValTrpMetGlyThrTrpAsnG 291
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872 GTACACACAGAGGTGGCCATCAAAACCTGAAAGCCTGGACAGATGTCCCA 921
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291 LysThrLysValAlaValLysThrLeuLysProGlyThrMetSerPro 307
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922 GAGCGCTTCTCGCAGAGAGCCAGTCAATGAGAGCTGAGCATGAGAA 971
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308 GlnAlaPheLeuGlnGlnAlaGlnIleMetLysArgLeuArgHisAspLys 324
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
972 GCTGTGCGAGTTGTATGCTGTGTTCAGAGAGGCCATTATCATGCTCA 1021
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324 sLeuValGlnLeuTyraValAlaValSerGlnGlnProIleTyTrIleValT 341
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1022 CGGAGTACATGAGCAAGGAGAGTTGCTGACCTTGTCCAGGGGGAGACA 1071
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341 heGlnPheMetSerGlnGlySerLeuLeuAspPheLeuLysAspGlyAsp 357
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1072 GGCACATACCTGGCGCTGCTCAGCTGTGTGACATGGCTGCTAGATCGC 1121
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358 GlyArgTyLeuLysLeuProGlnLeuValAspMetAlaAlaGlnIleAl 374
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374 AlaGlyMetAlaTyTrIleGlnArgMetAsnTyTrIleHisArgAspLeuA 391
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391 rGlnAlaAsnIleLeuValGlyAspAsnLeuValLysLysIleAlaAsp 407
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1222 TTTGGGCTGCTCGGCTCATTTGAAGACAAATGATACACGCGCGGCAAG 1271
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408 PheGlyLeuAlaArgLeuIleGlnAspAsnGlnTyTrThrAlaArgGlnI 424
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1272 TGCCAAATTCCTCATAGTGAAGGCTCCAGAGTCCCTGTATGGCC 1321
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424 yAlaLysPheProIleLysTrpThrAlaProGlnAlaAlaLeuPheGlyL 441
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
1322 GCTTACCATCAAGTGGAGCTGTGCTCTTCCGGATCCCTGCTGACTGAG 1371
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441 yAspThrIleLysSerAspValTrpSerPheGlyIleLeuLeuThrGln 457
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458 LeuValThrLysGlyArgValProTyProGlyMetAsnAsnArgGlnVal 474
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1422 GCTGACACAGGTGAGCGGGGCTACCGGATGCCCTGCGCCGCGAGTGT 1471
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
474 IleuGlnGlnValGlnArgGlyTyraArgMetGlnCysProGlyGlyCysP 491
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
1472 CCGAGTCCCTGACACGACCTCATGTGCCATGTCTGGCGGAGAGGCTGAG 1521
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
491 rOPserLeuHisAspValMetValGlnCysTrpLysArgGlnProGln 507
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
1522 GAGCGGCGCACCTTGCAGTACCTGACGAGGCTTCTGGAGAGCACTTTCAC 1571
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
508 GlnArgProThrPheGlnTyTrLeuGlnSerPheLeuGlnLysPyrPheTh 524
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
1572 GTCCACCGAGCCCATACAGCCCGGAGAGAAC 1605
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1022 CGGAGTACATGAGCAGGAGGAGTTGCTGACCTTCTCAAGGGGAGACA 1071
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341 hrluphemetserglnlyserleuaspheleuysaspdlyasp 357
1072 GGCAGAGACCTGGCGGCTGAGCTGAGTGGCTGCTGCTGAGTGGC 1121
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358 GLYhrgrtyrleuysleuproglnleuvalaspmetalaaglnlleal 374
1122 CTCAGGACATGCGCTGAGTGGAGGATGAATACGTCACCGGAGACTTC 1171
|||||
374 aalaglymetalatyrillegluarqmetasnlyllehislrqaspleua 391
1172 GTCAGACCAATCTCTGCTGGGAGAGAACTGTGTGCAAGTGGCCGAC 1221
|||||
391 rglalaalaasnilleuvalglaspasnleuvalcyslysllealasp 407
1222 TTGGGGTGGCTGGCTCATTTGAAGACAATGATGACAGCGCGGCAAG 1271
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408 Pheglyleuvalaargleuilegluaspsnslutyrthrilaarglnl 424
1272 TGGCAATTCCTCATCAAGTGGAGGCTCCAGAGCTGCCCTCATGGCC 1321
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424 yalalyspheproilleystprfhralaproglualalaalendpneglyl 441
1322 GCTTCACCATCAAGTGGAGTGGTGTCTTGGGATCCTGCTGACTGAG 1371
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441 yshethrilleysersaspvaltrpserpneglylleuendhrhglu 457
1372 CTCACCAAGAGGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1421
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458 leuvalthrlysglyarqvalprotyrproglymetasnlnaarglnua 474
1422 GCTGAGACAGGAGGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1471
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474 lleuglnlgnvalgluarqglytyrarqmetglnlcyssproglyslcysp 491
1472 CCGAGTCCCTGACAGCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1521
|||||
491 roproserleuuhlsaspvalmetvalglnlcystrplysarqglnproglu 507
1522 GAGCGGCCCCACTTCGAGTACCTGACGAGCTTCTGAGAGGACTACTTAC 1571
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508 gluarqprothrphnegluylrleuglnserpneleuulnsplyrpheth 524
1572 GTCACCGAGAGCCCCAGTACCAAGCCCCGGGAGAAC 1605
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seq_name: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:US-08-594-447-1

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seq_documentation_block:
: Sequence 1, Application US/08594447
: Patent No. 5776716
: GENERAL INFORMATION:
: APPLICANT: Ron, Dorit
: APPLICANT: Napolitano, Eugene W.
: APPLICANT: Voronova, Anna F.
: TITLE OF INVENTION: METHODS FOR IDENTIFYING AGENTS WHICH
: TITLE OF INVENTION: BLOCK THE INTERACTION OF FYN WITH PKC-THETA, AND USES
: NUMBER OF SEQUENCES: 75
: CORRESPONDENCE ADDRESS:
: ADDRESS: MORRISON & FOERSTER
: STREET: 2000 Pennsylvania Avenue, NW - Ste. 5500
: CITY: Washington
: STATE: DC
: COUNTRY: USA
: ZIP: 20006-1888
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30

```

```

CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/594,447
: FILING DATE: 31-JAN-1996
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Murashige, Kate H.
: REGISTRATION NUMBER: 29,959
: REFERENCE/DOCKET NUMBER: 22550-20025.24
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 887-1500
: TELEFAX: (202) 822-0168
: TELEX: 90-4030 MRSNFOERSM
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 532 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-08-594-447-1

alignment_scores:
: Quality: 1944.00 Length: 550
: Ratio: 4.208 Gaps: 7
: Percent Similarity: 84.000 Percent Identity: 68.545

alignment_block:
: US-09-444-711-1 x US-08-594-447-1
Align seg 1/1 to: US-08-594-447-1 from: 1 to: 532

1 ATGGGTACCAACAGAGCAAGCCCAAGATGCCAGGACGCGCGGCGAG 50
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1 Metgilycysvalglnlcysslyspysglualalaala.....lyslenth 15
51 COTGAGCGCGCGGAGAGAGCTGACGAGCGCGCGCGCGCGCGCTTCCCG 100
|||||
15 rgluulnargaspnglyserleuasnlnsersegltyrarqtyrlygl 32
101 COTGCAACACCCGAGAGCCAGGACGCTCG..... 129
|||||
32 hrasprprothrprolnlthtyrproserpneglyvalthrserlepro 48
130 .....GCGAGCGCCACCGCGCGCGCGCGCGCGCTT 161
|||||
49 Asnlyrasnlnasnlnalalalagllyglnglyleuthr..... 62
162 CGCCCGCGCGCGCGCGAGCCGAGCTGTGCGAGGCTTCACTCTCGG 211
|||||
63 .....Valpneglylgluvalasnserse 71
212 AC...ACCGTACCTCCCGGAGGCGCGCGCGCGCGCTGCGCGGAGAG 258
|||||
71 ernlsthrglythleuargthrarglyglythr.....glyal 84
259 AACACCTTTGTGCGCTGATGACTATGAGTGTAGACGAGAGACGCT 308
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85 Thrleuphevalalaleuvaltyrptyr...Alaargthrglnaspspe 100
309 GTCTTCAAGAGGAGCGGCGCTCAGATTGTCAACAACAGCGAGGAG 358
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100 userpnehlslsglyglulyspnehlilleuasnlnserseglugly 117
359 ACTGCTGCTGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 408
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117 sptrprrpnlalargserleuonthrnglylthrglyltyrlllepro 133
409 AGCACTAGTGGCGCGCTGCGACTTCATCCAGCGTGGAGAGTGTATT 458
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459 TGGCAAGATCACCAAGCGGAGTCAAGCGGCTTACTGCTCAATGACAG 508

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Percent Similarity: 83.962 Percent Identity: 67.170

alignment_block:

US-09-444-711-1 x US-08-426-509A-15

Align seg 1/1 to: US-08-426-509A-15 from: 1 to: 529

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   LysLeuGluProValAlaThrAlaLysGluAspAlaGlyLeuGluGlyAs 24
63 CGAAGACGTGCACGCGCTGGCGGGGCGCTTCCCGCCTCCGACGCC 112
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   24 pHeaATSerTyrGlyAlaAlaAspHisTyrGlyPro...AspProThrL 40
113 CGAGCAAGCGAGCTGGCGGCGGAGCGGCGGCGGCGGCGGCGCTTC 162
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   40 ysaAlaArgProAlaSerSerPheAlaHisIleProAsnTyrSerAsn 56
163 GCCCGCGCGCGCGCGCGAGCCCAAGCTGTTGAGGCTTCAACTCCTCG 212
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   57 SerSerGlnAlaIleAsnPro.....GlyPheLeuAspSerG 69
213 CACCGTCACCTCCCGCAGAGGCGGCGCGCTGGCGGCTGAGTACCA 262
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   69 yThrIle.....ArgGlyValSerGlyIleGlyValThrL 81
263 CCTTTGTGGCCCTCTATGACTATGACTAGCTAGAGGAGAGACACTTCC 312
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   81 eupHeIleAlaLeuTyrAspTyrGluAlaArgTyrGluAspPleuThr 97
313 TTCACAAAGAGCGAGCGGCTCCAGATTGTACACACAGCGAGGAGACTG 362
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   98 PheThrLysGlyGlyLysPheHisIleLeuAsnHisThrGluGlyAsp 114
363 GTGGCTGGCCCACTCGCTCAGACAGAGACAGAGAGGCTTACATCCCG 412
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   114 pTrpGluAlaArgSerLeuSerSerGlyLysThrGlyCysIleProSe 131
413 ACTACGTGGCGGCTCCGACTCCATCCAGGCTGAGAGGTGATATTTGG 462
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   131 snTyrValAlaProValAspSerIleGlnAlaGluGluTyrPheGly 147
463 AAGATACAGAGAGGAGTGCAGAGCGGTTACTGTCATGCAAGAGAAC 512
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   148 LysIleGlyArgLysAspAlaGluArgGluLeuLeuSerProGlyAsn 164
513 GAGAGGAGCTTCTCGTCGAGAGAAAGTGAACACAGAAAGTGCCTACT 562
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   164 oGlnGlyAlaPheLeuIleArgIleSerGluThrThrLysGlyAlaTyr 181
563 GCCTCTAGTGTGACTTGCAGAACGCCAAGGCGCTCAAGGTGAGAAC 612
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   181 erLeuSerIleArgAspTyrPheGlnThrArgGlyAspHisValLys 197
613 TACAAATCCGCAAGCTGAGACAGCGGCGCTTACATCACTCCCGCAC 662
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   198 TyrLysIleArgLysLeuAspMetGlyLysTyrIleThrThrArgVa 214
663 CCAAGTTCACAGCGCTGACAGAGCTGTGGCGCTACTACTCCAAACGCG 712
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   214 IGIlnPheAsnSerValGlnGluLeuValGlnHisTyrMetGluValAs 231
713 ATGGCTGTCCACCGCTCACCACCGTGTGCGCCACGCTCCAGCGCGAG 762
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   231 spGlyLeuCysAsnLeuLeuIleAlaProCysThrIleMetLysProG 247
763 ACTCAGGCGCTGGCCAAAGATGCCCTGGAGATCCCTCGGAGTGCCTCG 812
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   248 ThrLeuGlyLeuAlaLysAspAlaTyrGluIleSerArgSerSerIle 264
813 GCTGAGAGTCAAGCTGGCGCGAGGCTGTTGGCAGAGTGTGATGGAGA 862
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264 rLeuGluAlaArgLysLeuGlyThrGlyCysPheGlyAspValThrPLeuGly 281
863 CCTGGAAGGTATCCACAGAGGTGGCCATCAAAACCTGAAGGCTGGACG 912
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   281 hTrpAsnGlySerThrLysValAlaValLysThrLeuLysProGlyThr 297
913 ATGTCTCCAGAGGCTTCTCCAGGAGGCGCCAGCTCATGAGAACGTGAG 962
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   298 MetSerProLysAlaPheLeuGluGluAlaGlnValMetLysLeuLeu 314
963 GCATGAGAAAGCTGGTGCAGTGTATGCTGTGCTTCAAGAGGCCATTT 1012
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   314 gHisAspLysLeuValGlnLeuTyrAlaValValSerGluGluProIle 331
1013 ACATGTCACGAGATGATGAGCAAGGGAGATGCTGAGACTTGTTCAG 1062
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   331 yTlleValThrGluPheMetCysHisGlySerLeuLeuAspPheLeu 347
1063 GGGGAGACAGGCCAAGTACCTCGCGCTGCCTCAGCTGATGACATGCTGC 1112
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   348 AsnProGluGlyGlnAspLeuAlaArgLeuProGlnLeuValAspMet 364
1113 TCAGATGCTCTCAGGCAATGGCGGTACGTGAGCGGATGAATACGTCC 1162
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   364 aGlnValAlaGluGluMetAlaTyrMetGluArgMetAsnTyrIleHis 381
1163 GGGACCTTGTGCAAGCCAAATCTCGTGAGGAGAGAACCTGTGTGCA 1212
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   381 rGAspLeuAlaAlaAlaAsnIleLeuValGlyGluArgLeuAlaCys 397
1213 GTGGCGGACTTGGGCTGGCTCGGCTCATTTGAAGCAATGAGTACAGCG 1262
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   398 IleAlaAspPheGlyLeuAlaArgLeuIleLysAspAspGluTyrAsn 414
1263 GCGGCAAGGTCCAAATTCGCCATCAAGTGAAGGCTCCAGAGTGC 1312
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   414 oCysGlnIleLysLysPheProIleLysTyrPheAlaProGluAlaAl 431
1313 TCTATGGCGCTTACCATCAAGTGAAGTGTGTCTTGGGATCCTG 1362
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   431 eupHeGlyArgPheThrIleLysSerAspValTyrSerPheGlyIle 447
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   448 LeuThrGluLeuIleThrLysGlyArgIleProTyrProGlyMetAsn 464
1413 CCGGAGAGTGTGACACAGTGAAGCGGCGCTACCGAGTCCCTGCCGC 1462
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   464 sArgGluValLeuGluGlnValGluGlnGlyThrHisMetProCysPro 481
1463 CGAGGTGCCGAGTCCCTGCACGACCTCATGTGCTGCTGGCGGAG 1512
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   481 roGlyCysProAlaSerLeuTyrGluAlaMetGluGlnThrTrpArg 497
1513 GAGCTGAGAGAGCGGCCACCTTGCAGTACCTGCAAGGCTTCTTGAGAG 1562
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   498 AspProGluGluArgProThrPheGluTyrLeuGlnSerPheLeuGln 514
1563 CTACTTCAAGTCCACGAGCCCGCATACAGCCGCGGAG 1602
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   514 pTyrPheThrSerAlaGluProGlnTyrGlnProGlyAsp 527

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XX 28-MAY-1999; 99MO-US11780.
XX
XX 29-MAY-1998; 98US-0087220.
XX

XX (SCRI) SCRIPPS RES INST.
XX

XX Cheresch DA, ElliceIri B, Schwartzberg PL;
XX

XX WPI; 2000-116335/10.
XX

XX N-PSDB; AA229700.
XX

XX Using tyrosine kinase Src for modulating angiogenesis in tissues useful
XX in, e.g. treatment of chronic articular rheumatism -

XX Claim 1; Fig 2; 80pp; English.
XX

XX The present sequence is the wild-type chicken c-Src tyrosine kinase.
XX This Src protein can be used to modulate angiogenesis. When the Src
XX protein is inactivated, angiogenesis is inhibited while, when it is
XX activated, angiogenesis is potentiated. The modified or variant Src can
XX be used to treat inflammatory diseases like, arthritis, rheumatoid
XX arthritis, diabetic retinopathy, restenosis, osteoporosis and cancer
XX associated disorders.

XX Sequence 533 AA;

alignment_scores:

Quality: 2663.50 Length: 536
Ratio: 5.112 Gaps: 1
Percent Similarity: 97.201 Percent Identity: 94.030

alignment_block:

US-09-444-711-1 x AA444447 ..

Align seg 1/1 to: AA444447 from: 1 to: 533

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1 MetGlySerSerLysSerLysProLysAspProSerGlnArgArgLys 17
51 CCTGAGCGCGCGAGACGTGACGCGCGCGCGCGCGCGCGCGCGCG 100
17 IleuGlnProProAspSerThrHis.....HisGlyGlyPhePro 31
101 CCTGCAGACCGCCGAGACAGCCAGCCTGCGCGCGCGCGCGCGCG 150
31 AsnGlnThrProAsnLysThrAlaAlaProAspThrHisArgThrPro 47
151 AGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 200
48 SerArgSerPheGlyThrValAlaThrGluProLysLeuPheGly 64
201 CAATCTCTCGACACCGTCACTCCCGCGAGAGCGCGCGCGCGCGCG 250
64 AsnThrSerAspThrValThrSerProGlnArgAlaGlyAlaLeuAla 81
251 GTGGAGGTGACACCTTGTGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
81 LysIleValThrThrPheValAlaLeuThrAspTyrGluSerArgThrGlu 97
301 ACAGACCTGCTCTCAGAAAGCGAGCGCGCGCGCGCGCGCGCGCG 350
98 ThrAspLeuSerPheLysLysGlyGluArgLeuGlnIleValAlaAsn 114
351 GGAGGAGACGTGGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 400
114 rGluGlyAspTrpTrpLeuAlaHisSerLeuThrGlnGlnThrGly 131
401 ACATCCCGACAACTACGTGGCGCGCGCGCGCGCGCGCGCGCGCG 450
131 yTrIleProSerAsnTyrValAlaProSerAspSerIleGlnAlaGlu 147

451 TGGTATTTGGCAAGATCACCAGACGGAGTGCAGAGCGGTTACTGCTCA 500
148 TrpTyrPheGlyLysIleThrArgArgLysSerGlnArgLeuLeuAs 164
501 TGCAGAGAACCCGAGAGGACCTTCTCTGTCGCGAGAAAGTGAGACCA 550
164 nProGluAsnProArgLysThrPheLeuValArgGlnSerGlnThrTr 181
551 AAGGTGCTTACTGCTCTCACTGCTGCTGCTGCTGCTGCTGCTGCT 600
181 yGlyAlaTyrCysLeuSerValSerAspPheAspAlaLysGlyLeu 197
601 AAGGTGAGACATACAGATCCGACGCGCGCGCGCGCGCGCGCGCG 650
198 AsnValLysHisTyrLysIleArgLysLeuAspSerGlyGlyPheT 214
651 CACCTCCCGCACCCAGTTCACAGACCTGACAGACCTGCTGCTTACT 700
214 eThrSerArgThrGlnPheSerSerLeuGlnGlnLeuValAlaTyr 231
701 CCAACACGCGGATGCGCTGCGCGCGCGCGCGCGCGCGCGCGCG 750
231 eLysHisAlaAspGlyLeuGlnHisArgLeuThrAsnValLysPro 247
751 TCCAGCGCGGACGCTCAGCGCGCGCGCGCGCGCGCGCGCGCGCG 800
248 SerLysProGlnThrGlnGlyLeuAlaLysAspAlaTrpGluIle 264
801 GGAATGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 850
264 gGluSerLeuArgLeuGlnValLysLeuGlnGlnCysPheGlyGlu 281
851 TGTGATGGGACCTGAGACGATACACAGGATGCGCGCGCGCGCG 900
281 aLTrpMetGlyThrTrpAsnGlyThrArgValAlaIleLysThrLe 297
901 AAGCTGCGACGATGCTCTCCAGAGCGCTCTCTGCGAGGCGCGCG 950
298 LysProGlyThrMetSerProGlnAlaPheLeuGlnGlnAlaGln 314
951 GAAGAAGCTGAGCGATGAGAGCGGTGCGAGTGTGCTGCTGCTG 1000
314 tLysLysLeuArgHisGlyLysLysValGlnLeuTyrAlaValSer 331
1001 AGGAGCCATTTTACATGCTCAGGAGTACATGAGCAAGGAGTTGCT 1050
331 LysGluProIleTyrIleValThrGlnTyrMetSerLysGlySerLe 347
1051 GACTTTCTCAAGGGGAGACAGGACGATGCTGCGCGCGCGCGCG 1100
348 AspPheLeuLysGlyLysMetGlyLysTyrLeuArgLeuProGln 364
1101 GGACATGCTGCTCAGATGCTGCTCAGGCGATGCTGCTGCTGCTG 1150
364 LaspMetAlaAlaGlnIleAlaSerGlyMetAlaTyrValAlaG 381
1151 ACTAGTCCACCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1200
381 snTyrValHisArgAspLeuArgAlaAlaAsnIleLeuValGlyL 397
1201 CTGGTGTGCAAAAGTGGCGCGCGCGCGCGCGCGCGCGCGCGCG 1250
398 LeuValLysLysValAlaAspPheGlyLeuAlaArgLeuIleGlu 414
1251 TGAGTACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1300
414 nGluTyrThrAlaArgGlnGlyAlaLysPheProIleLysTrpThr 431
1301 CAGAAAGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1350
431 rGluAlaAlaLeuTyrLeuArgPheThrIleLysSerAspValTrp 447

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601 AACGTGAAGCACTACAGATCCGACAGCTGACAGCGCGGCTTACAT 650
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198 AsnVallyshIstYllyslleArlyslleuAspserGlyglYphenylrll 214
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651 CACCTCCCGCACCCAGTTCAACAGCCCTGCAGACAGCTGGTGGCTTACT 700
    |||||
214 eThrserrArghrInpHeserSerleuInglInleuValAlaIatYrYrs 231
    |||||
701 CCAACACAGCGGATGGCGCTGTCACCGCCCTGCACACCGTGGCCGACG 750
    |||||
231 eRlyshIAlaAspIleucYshIAsrGleuThrAsnValCysProthr 247
    |||||
751 TCCACAGCCGACAGACTCAGAGCGCTGGCCACAGATGCTGGAGATCCCTG 800
    |||||
248 SerlysprogInThrgInglYleuAlaIysAspAlatrpGlnIleproAr 264
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801 GGAGTCGCTGGCGGCTGAGAGCTGAGCTGGGCCAGGGGCTGTTGGCGAG 850
    |||||
264 gGluserleuArghleuGluValIlyslleuGlYnglYcysPheglYgluY 281
    |||||
851 TGTGTATGGGACCTGGAACGCTTACCACAGGGTGGCCATCAAAACCTG 900
    |||||
281 aItrpMeGlYThrrtrpAsnglYThrrArGValAlaIleuYsthrleu 297
    |||||
901 AAGCCTGGACGATGTCACAGGCGCTTCGACAGAGGCCAGGTCAT 950
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298 LysprogIYthrMetSerProgluAlaPheleuGlnIuAlaGlnVala 314
    |||||
951 GAAGAACGTCAGAGCATGAGAACCTGGTCAGTGTATGCTGTGTTTTCAG 1000
    |||||
314 tLyslYslleuArghIsgIuYslleuValGlnleuYrAlaValIValSerG 331
    |||||
1001 AGAAGCCATTATCATGCTCAGGAGTACATAGACAAGGGAGTTGCTG 1050
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331 lUgluProIleYrIleValThrgIuYrMetSerIysglYserleu 347
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1051 GACTTTCACAGAGGGGACAGGACAGGACATCTGGCGCTCCTCAGCTG 1100
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348 AspPheleuYsgIyluMetGlYstYrleuArghleuProglInleuVal 364
    |||||
1101 GGACATGGCTGCTGATGATGCTCAGGCGATGGCTACGTCAGGCGATGA 1150
    |||||
364 lAspMetAlaAlaGlnIleAlaSerGlYMetAlaIYrValGlnuArghMet 381
    |||||
1151 ACTACGTCACCGGAGCTTCGTCAGCCACATCTCGTGGGAGAGAAC 1200
    |||||
381 snYrYValHIsArghsPleuArghAlaAlaAsnIleleuValGlyluAsn 397
    |||||
1201 CTGGTGTGCAAAAGTGGCGACTTTGGGCTGGCTCGCTATTGAAAGACA 1250
    |||||
398 leuValCysIysValAlaAspPheglYleuAlaArghleuIleGluAsp 414
    |||||
1251 TGAGTACAGGGGCGGCAAGGTGCCAAATTGCCATCAAGTGGAGCGGTC 1300
    |||||
414 ngluYrThrrAlaArghInglYAlaIysPheProIlelysttrpThAla 431
    |||||
1301 CAGAAGCTGCCCTTCTGAGCGCTTACCATCAAGTCAGAGCTGTGGTCC 1350
    |||||
431 rogluAlaAlaIleuYrghYArghPheThrlIeYserAspAlaItrpSer 447
    |||||
1351 TTCGGGATTCCTGCTAGTGAAGTCAACACAAAGGACGGGCTCCCTACCC 1400
    |||||
448 PheglYIleleuIleuThrgIuIleuThrrIysglYArGValaProtyrPr 464
    |||||
1401 TGGATGTGTAACCGGAGGTGCTGACAGGTCGAGCGGGGCTACCGGA 1450
    |||||
464 oGlyMetValAsnArghGluValleuAspGlInValGlnuArghYrArgh 481
    |||||
1451 TGCCCTGGCCGCGGAGTGTCCCGAGTCCCTCAGACAGCTCATGTGCCAG 1500
    |||||
481 etProCyprProgluYsProgluSerleuHIsAspIleuMetCysGln 497

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1501 TGCTGGCGGAAGAGACCTGAGGAGCGGCCACACTTCGATGACTGCAGGC 1550
    |||||
498 CysTrpArghArghsProgIuGlnArghProThrPhegluYrIleuGlnAl 514
    |||||
1551 CTTCCTGGAGAGACTACTACGTCACCGGACCGCCCACTACACGCGCGGG 1600
    |||||
514 aPheleuGluAspYrPheThrrSerThrgIuProglInYrGlnProglYg 531
    |||||
1601 AGAACCTC 1608
    |||||
531 lUnsnleu 533

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seq_name: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:AAV44449
seq_documentation_block:
ID AAV44449 standard: Protein: 533 AA.

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AC AAV44449;
XX
XX
XX 22-MAR-2000 (first entry)
XX
XX

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DE Mutant chicken c-Src tyrosine kinase, SrcA.
XX
XX Angiogenesis; tyrosine kinase; Src; inhibition; activation; modulate;
KW chicken; mutant Src; SrcA; point mutation; Y527F; phosphorylation;
KW negative regulation; tyrosine; inflammatory disease; osteoporosis;
KW rheumatoid arthritis; diabetic retinopathy; restenosis; cancer.
XX
XX Gallus sp.
OS
XX Synthetic.
XX

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FT Key location/Qualifiers
FT Misc-difference 527 /label= Y527F
FT FT /note= "Wild type Tyr replaced with Phe"
XX
XX PN W09961590-A1.
XX
XX PD 02-DEC-1999.
XX
XX PF 28-MAY-1999; 99WO-US11780.
XX
XX PR 29-MAY-1998; 98US-0087220.
XX
XX PA (SCRI ) SCRIPPS RES INST.
XX
XX PI Cheresch DA, Elliceirl B, Schwartzberg PL.
XX
XX DR WPI: 2000-116335/10.
XX

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XX Using tyrosine kinase Src for modulating angiogenesis in tissues useful
XX in, e.g. treatment Of chronic articular rheumatism -
XX
XX PS Claim 3; Page -: 80pp; English.
XX
XX The present sequence is the mutant chicken c-Src tyrosine kinase,
XX SrcA. This sequence has a point mutation, Y527F, to activate c-Src.
XX This site is involved in negative regulation by the kinase CSK.
XX Phosphorylation of Tyr residue at 527 inactivates the protein. But in
XX the mutated SrcA, the regulatory Tyr is replaced with Phe, thus
XX constitutively activating the protein. This mutant Src protein can be
XX used to modulate angiogenesis. When the Src protein is inactivated,
XX angiogenesis is inhibited while, when it is activated, angiogenesis is
XX potentiated. The mutant or variant Src can be used to treat inflammatory
XX diseases like: arthritis, rheumatoid arthritis, diabetic retinopathy,
XX restenosis, osteoporosis and cancer associated disorders.
XX Note: This sequence is not found in the specification, but derived
XX from the sequence in Fig 2.

```

```

SQ Sequence 533 AA;

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```

alignment_scores:

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AC AAR39705;
 XX
 DT 23-DEC-1993 (first entry)
 XX
 DE Chicken pp60 c-src protein.
 XX
 KW Endothelial; tyrosine kinase protein; pp60 c-src; ss.
 XX
 OS Gallus gallus.
 XX
 PN MO9314193-A.
 XX
 PD 22-JUL-1993.
 XX
 PF 05-JAN-1993; 93MO-US00445.
 XX
 PR 06-JAN-1992; 92US-0820011.
 XX
 (UYVA) UNIV YALE.
 XX
 PI Bell L, Luthringer DJ, Madri JA, Warren SL.
 XX
 DR WPJ; 1993-243209/30.
 XX
 DR P-PSDB; AAR39705.
 XX
 PS Genetically engineered endothelial cells - which exhibit enhanced
 XX cell migration, urokinase-type plasminogen activator activity,
 XX and reduced mononuclear cell adhesion and fibronectin prodn
 XX
 PS Disclosure; Page 64-66; 91pp; English.
 XX
 CC The DNA encoding a portion or (more preferably) the entire pp60
 XX c-src polypeptide (Given in AA046687) is used to transform endothelial
 XX cells. Transformed cells produce increased amounts of pp60 c-src and
 XX have improved therapeutic properties. They migrate at faster rates
 XX than non-transformed counterparts; have an enhanced ability to
 XX inhibit the formation of thrombi and/or dissolve thrombi once they
 XX have formed and exhibit reduced mononuclear cell adhesion. They can
 XX also be used to improve the success of surgical procedures such as
 XX coronary angioplasty, heart bypass surgery, vessel graft and stent
 XX implantation.
 XX
 SO Sequence 533 AA;
 XX
 Alignment_scores: Length: 536
 Quality: 2658.50 Gaps: 1
 Ratio: 5.103
 Percent Similarity: 97.201 Percent Identity: 93.843
 Alignment_block:
 US-09-444-711-1 x AAR39705 ..
 Align seg 1/1 to: AAR39705 from: 1 to: 533

64 eAsnThrSerAspThrValThrSerProGlnArgAlaLeuAlaG 81
 251 GTGAGTGAACACCTTTGTGGCCCTATGACTATGATCTAGACGGAG 300
 81 LgLYValThrThrPheValAlaLeuThrAspTyrGluSerArgThrGlu 97
 301 ACAGACCTTCCTTCAGAAAGGCGGCGCTCCACATTGTCAACAAC 350
 98 ThrAspLeuSerPheLeuSylgIuArgLeuGlnIleValAlaAsnThr 114
 351 GGAGGAGACGTGTGGCTGGCCACTCGCTCAGACAGACAGACAGGCT 400
 114 rGluGluAspTrpTrpLeuAlaHisSerLeuThrThrGlnThrGlyT 131
 401 ACATCCCGACGACTACGTGGCGCCCTCCGACTCCATCCAGGCTGAG 450
 131 YrIleProSerAsnTyrValAlaProSerAspSerIleGlnIleGlu 147
 451 TGGTATTTTGGCAAGATCACAGACGAGGAGTGCAGAGCGGTACTGCT 500
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 501 TGCAGAGAACCCGAGAGGAGACCTTCCTCGTGGAGAAATGAGACCA 550
 164 nProGluAsnProArgGlyThrPheLeuValArgGluSerGluThrThr 181
 551 AAGTGGCTACTAGCTCTGCTGAGTGTGACTTCGACAAACCCAGGCTC 600
 181 YsGlyValArgCysLeuSerValSerAspPheAspAsnAlaLysGly 197
 601 AACGTGAAGCACTACAAAGATCCGCAAGCTGGACAGCGCGGCTTCAC 650
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 214 eThrSerArgThrGlnPheSerSerLeuGlnGlnLeuValAlaTyrLys 231
 701 CCAACACGCGCATGAGCGCTGTGCCACCGCTCAGCACCGTGGCCAC 750
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 851 TGTGATGGGAGACTGGAACGGTACCACAGGAGGTGGCCATAAACCC 900
 281 alTrpMetGlyThrTrpAsnGlyThrThrArgValAlaIleLysThrLeu 297
 901 AAGCTGGACGATGTCTCCAGAGGCTTCTGCAGAGAGGCCAGGTCAT 950
 298 LysProGlyAsnMetSerProGluAlaPheLeuGlnGluAlaGlnVal 314
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 314 TrpLysLeuArgHisGluLysLeuValGlnLeuTyrAlaValAlaSer 331
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551 AAGTGCCTACTGCTCTCAGTGTCTACTTTCAGCAACGCCAAGGCGCTC 600
181 ySeGlyAlaTyrcysLeuSerValSerAspPheAspAlaIleGlyLeu 197
601 AACGTGAAGCACTACAAGATCCGCAACCTGGACAGCGCGGCTTACAT 650
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264 gGluSerLeuArgLeuGlnValIleuGlyGlnIleCysPheGlyGluV 281
851 TCGGATGGGAGCTGGAACGTACCAACCGAGGCGGCATCAAAACCTG 900
281 alrPheGlyIleThrPasnGlyThrThrArgValAlaIleMetThrLeu 297
901 AAGCTGCGCAGATGTCTCCAGAGGCTTCTGACAGAGGCGCCAGTCA 950
298 LysProGlyIleThrMetSerProGluAlaPheLeuGlnIleuAlaIle 314
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1301 CAGAGAGTCCCTCTATGGCGGCTTACCACTCAAGTGGAGCTGTGCTC 1350
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481 eTrpCysProProGluIleuSerProGluSerLeuHisAspLeuMetCysGln 497
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1551 CTCTCGAGAGCACTTCTCAGCTCCAGCGAGCCCGCAGTACAGCCCGGGG 1600
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1601 AGAACCTC 1608
531 lAsnIleu 533

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ABG23778:
AC
XX
XX
DT 18-FEB-2002 (first entry)
DE
XX
XX
DE Novel human diagnostic protein #23769.
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
OS Homo sapiens.
XX
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001MO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YF.
XX
DR N-PSDB; AAS87965.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity
XX
PS Claim 20: SEQ ID No 54137; 103pp: English.
XX
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating

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1 MetGlyCysIleLeuSerLysGluAsnLysSerProAlaIleLysTyrAr 17
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17 pProGluAsnThrProGluProValSerThrValSerHisTyrGlyA 34
92 CTTTCCCGCGCTGCAGACCCCGACCAAGCCAGCTCGCGGACGGCCAC 141
34 IacIuProThrThrValSerProCysProSerSerSerAla..... 47
142 CCGGGCCCCAGCGCGCTTCGCCCGCGCGCGCGACGCC..... 183
48 LysGlyThrAlaValAsnPhSerSerLeuSerMetThrProPheGlyG 64
184 .....AAGCTGTCGAGAGCTCAACTCCTCGAGACCGCTCA 220
64 ySerSerGlyValThrProPheGlyGlyAlaSerSerSerPheSerVal 81
221 CTTCCCGCGAGAGGGCGCGCGCTGCAGGTGAGTACACCTTTGTG 270
81 alProSerSerTyrProAlaGlyLeuThrGlyValThrIlePheVal 97
271 GCCCTTATGATATGATGCTAGACAGAGACAGACCTGCTCTCAAGAA 320
98 AlaLeuTyrAspTyrGluAlaArgThrThrGluAspLeuSerPheLys 114
321 AGCGAGCGCGCTCCAGATTGTCAACAACAGCGAGGAGACTGTGGCTG 370
114 sGlyGluArgPheGlnIleIleAsnThrGluGlyAspTyrPheGlu 131
371 CCGACGCGCTCAGCAGACAGACAGACAGCTACATCCCGACGACTAG 420
131 laArgSerIleAlaThrGlyLysAsnGlyTyrIleProSerAsnTyrVal 147
421 GCGCCCTCCGACTCCATCCAGCTGAGAGAGTGTATTGGACAGATCAC 470
148 AlaProAlaAspSerIleGlnAlaGluGluTyrPheGlyLysMetG 164
471 CAGACGGGAGCTCAGAGCGGTACTGCTCAATGCAGAACCCGAGAGGA 520
164 yArgLysAspAlaGluArgLeuLeuAsnProGlyAsnGlnArgGly 181
521 CCTTCTCGCGGAGAAAGTGAGACCAAGAGTGCCTACTGCTCTCA 570
181 lePheLeuValArgGluSerGluThrThrLysGlyAlaTyrSerLeu 197
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621 CCGCAAGCTGGAGACGGCGGCTTACATCACCTCCGACACCAAGTTCA 670
214 eArgLysLeuAspAsnGlyGlyTyrIleThrThrArgAlaGlnPhe 231
671 ACAGCTGACAGAGCTGTGGCTACTACTCAACAACGCGCATGGCTG 720
231 sPheThrLeuGlnLysLeuValLysHisTyrThrGluHisAlaAspGly 247
721 TGGCAGCGCTACCAACCGTGTGCCCGACGTCAAGCCGCGACTCAAG 770
248 CysHisLysLeuThrThrValCysProThrValLysProGlnThrGln 264
771 CCGGCGCAAGATGCTGGAGATCCCTCGGAGCTCGCTCGCGCTGAGG 820
264 yLeuAlaLysAspAlaTyrGluIleProArgGluSerLeuArgGlu 281
821 TCAGAGTGGGCGCAGGCTGCTTGGCGAGGTGTGATGGGAGCTGGAAC 870
281 alLysLeuGlnGlyCysPheGlyGluValTyrMetGlyThrPheAsn 297
871 GGNACACACGAGGTGGCATCAAAACCTGAAGCTGGCAGATGTCTCC 920
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298 GlyThrThrLysValAlaIleLysThrLeuLysProGlyThrMetLeu 314
921 AGAGGCTTCCTCGAGAGGCCAGGCTCATGAAGCTGAGCATGATA 970
314 oGluAlaPheLeuGlnGluAlaGlnIleMetLysLysLeuArgHisAsp 331
971 AGCTGGTCAGTTGTATGCTGTGTTCAGAGAGACCCATTACATCGTC 1020
331 yLeuValProLeuTyrAlaValAlaValSerGluGluProIleTyrIle 347
1021 ACGAGTACATGACGACAGGGAGCTTGTGACTTCTCAAGGGGAGAC 1070
348 ThrGluPheMetSerLysGlySerLeuLeuAspPheLeuLysGluGly 364
1071 AGGCAAGTACCTGGCGCTGCTCAGCTGTGACATGGTGTCTCAGATG 1120
364 pGlyLysTyrLeuLysLeuProGlnLeuValAspMetAlaAlaGlnIle 381
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381 laAspGlyMetAlaTyrIleGluArgMetAsnTyrIleHisArgAspLeu 397
1171 CGTGACGCCAACATCTGTGTGGAGAGAACTGTGTGCAAAAGTGGCG 1220
398 ArgAlaAlaAsnIleLeuValGlyGluAsnLeuValCysLysIleAla 414
1221 CTTTGGCTGGCTGGCTCATTTGAAGACATGATGACGCGCGGCGAAG 1270
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1371 GCTCACCAAAAGGAGGGGTGCTTACCTCGGATGTGAACCGGAGG 1420
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481 alLeuGlnGlnValGluArgGlyTyrArgMetProCysProGlnGly 497
1471 CCGGAGTCCCTGCACGACCTCATGTGCCAGTGTGCGGAGAGAGCTCA 1520
498 ProGluSerLeuHisGluLeuMetAsnLeuCysTyrPheLysAspPro 514
1521 GGAGCGGCCACCTTGAATCTGACAGGCTTCTGTGAGACTACTTCA 1570
514 pGluArgProThrPheGluTyrIleGlnSerPheLeuGlnAspTyrPhe 531
1571 CGTCCACCGGAGCCCGATACAGAGCCCGGGGAGAACCTC 1608
531 hrAlaThrGluProGlnTyrGlnProGlyGluAsnLeu 543
seq_name: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:AA1999
seq_documentation_block:
ID AA1999 standard; Protein: 543 AA.
AA1999:
AC AA1999 (first entry)
DT 23-SEP-1999
DE Human yeast protein.
XX Human; yes1; diagnosis; neuropsychiatric disorder; BAD; schizophrenia;
XX bipolar affective disorder; attention deficit disorder;
XX schizoaffective disorder; unipolar affective disorder;
XX Huntington's disease; Parkinson's disease; manic-depression.
KW

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|||||
398 ArgAlaAlaAsnIleLeuValGlyGluAsnLeuValCysIleAlaAs 414
|||||
1221 CTTTGGGCTGGCGGCTCATGTAACACATGATGATACAGCGCGCGGAG 1270
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431 lYAlaAlaSheProIleTyrThrAlaProGluAlaAlaLeuTyrGly 447
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1321 CGCTTCACCATCAAGTGAAGCGGTGTGCTTGGGATCCTGCTGACTGA 1370
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1371 GCTCAGCAAAAGGAGCGGTGCTTACCTGGGATGATGAGACCGGAGG 1420
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464 uLeuValThrLysGlyArgValProTyrProGlyMetValAsnArgGly 481
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1421 TGCCTGAGCAGGTGGAGCGGCTACCGGATGCGCCCGCGCGGAGTGT 1470
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1471 CCCGAGTCCCTCAGCAGCTCATGTGCCAGTGTGCGGAGAGACCTGA 1520
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498 ProGluSerLeuHisGluLeuMetAsnLeuCysTyrPlysAspProAs 514
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514 pGluArgProThrPheGluTyrIleGlnSerPheLeuGluAspTyrPhe 531
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531 hAlaThrGluProGlnTyrGlnProGlyGluAsnLeu 543
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seq_name: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:ABG23777
seq_documentation_block:
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ABG23777:
X.
DT 18-FEB-2002 (first entry)
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DE Novel human diagnostic protein #23768.
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KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
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OS Homo sapiens.
XX
PN M0200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001MO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
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PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
XX
DR N-PSDB; AAS87964.
XX

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PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
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XX
PS Claim 20; SEQ ID No 54136; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WPIO
CC at ftp.wipo.int/pub/published_pot_sequences.
XX
SQ Sequence 351 AA:

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  Ratio: 5.319          Gaps: 0
Percent Similarity: 100.000    Percent Identity: 100.000

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alignment_block:

US-09-444-711-1 x ABG23777 ..

Align seg 1/1 to: ABG23777 from: 1 to: 351

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|||||
17 lLysHisTyrLysIleArgPlysLeuAspSerGlyPheTyrIleThr 34
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656 CCCGACCCCAATTCAACAGCCTGCAGCAGCTGTGCGCTTACTACTCCAA 705
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34 eArgThrGlnPheAsnSerLeuGlnGlnLeuValAlaTyrTyrSerIys 50
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756 GCCGACAGCTCAGGGCGCTGGCCAAAGATGCCGTGGAGATCCCTGGGAGT 805
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84 eArgLeuArgLeuGlnValLysLeuGlnGlnGlyCysPheGlyGlyValTyr 100
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101 MetGlyThrTyrPAsnGlyThrThrArgValAlaIleLysThrLeuLysPr 117
|||||
906 TGGCAGATGTCTCCAGAGGCTTCTGCAGAGAGGCCAGGCTCATGAAGA 955
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117 oGlyThrMetSerProGluAlaPheLeuGlnGlnValGlnValMetLysL 134

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173 PAAPGlyGlyPhePheIleSerThrArgIleProPheProSerLeuProG 190
683 AGCTGTGGCTTACTACTCCAAACACCCGATGGCTGTGGCCACGGCTC 732
190 IuLeuValArgHisTyrGlnGlyValAspGlyLeuGlyGlnCysLeu 206
733 ACCACCGCTGGCCCCACCTCCACCGCCAGCTCAGGGCCCTGGCCAAAGA 782
207 ThrIleProCysGlnThrValArgProGlu...LysProThrGluLysAs 222
783 TGGCTGGAGATCCCTCGGAGATGCTGCGCTGAGCTCAGCTGAGGCC 832
222 PALATTPGluIleProArgIleSerLeuSerLeuGlnLysLysLeuGlyA 239
833 AGGCTGCTCTTGGCGAGTGTGATGGGAGACCTGAAACGGTACACACAG 882
239 IaGlyGlnPheGlyAspValThrLeuAlaMetTyrAsnGlyHisThrLys 255
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256 ValAlaValIlyshThrMetLysProGlySerMetSerProGlyAlaPheLe 272
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CC treatment and modulation of diseases, disease symptoms or the effect of
 CC other physiological events mediated by kinases, having one or more kinase
 CC enzymes involved in their pathology.
 XX

SO Sequence 508 AA:

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Quality: 1464.00 Length: 454
 Ratio: 3.812 Gaps: 3
 Percent Similarity: 84.581 Percent Identity: 59.912

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US-09-444-711-1 x AAB37700 ..

Align seg 1/1 to: AAB37700 from: 1 to: 508

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120 rLeuGlnProGluProTrpPhePheLysAsnLeuSerArgLysAspLag 137
485 AGCGGTTACTGCTCAATGCAGACAGACCGGAGACCTTCCTGCTGCGA 534
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585 CAACGCCAAGGCGCTCAAGTGAAGCACTCAAGATCCGACAGCTGACA 634
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635 GCGGGCGCTTACATCACCTCCCGACACCGAGTTCAAACGCTGCGAGC 684
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1035 CAAGGGGAGTTTGGCTGGAGCTTTCACAGGGGAGACAGACAGTACCTGC 1084
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1435 GAGCGGCGCTACCGGATGCCCTGGCGGAGTGGCTGCGGATGCCATCA 1484
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1485 CGACCTCATGTGCCAGTGTGGCGGAAAGAGCTGAGAGGCGGCCACCT 1534
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XX 13-MAR-2000 (first entry)
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XX PKA substrate, Src-family protein.
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XX Protein kinase A; PKA; PKA signaling pathway; phosphorylation; cancer;
XX kinase substrate; immunosuppressive disorder; proliferative disease;
XX HIV infection; AIDS; immunodeficiency; autoimmune disease;
XX systemic lupus erythematosus; Src-family.
OS Homo sapiens.

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509 ACCGAGAGAGGACCTTCTGCTGAGAAAGTGAACACGAGAAAGTGC 558
168 snProArgGlyThrPheLeuIleArgGlnSerGlnThrLysGlyAla 184
559 TACTGCTCTCAGTGTCTGACCTTGACACACGCCAAGGCGCTCAACGTGA 608
185 TyrSerLeuSerIleArgAspTrpAspMetLysGlyAspHisVal 201
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201 shsTyLysIleArgLysLeuAspAsnGlyLysTyLysIleThr 218
659 GCACCCGCTCAACAGCGCTGACAGCGTGGGCTTACTACTCAACAC 708
218 rgaIaGlnPheGlnThrLeuGlnIleuValGlnHisTyrSerGluArg 234
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351 uAspPheLeuLysAspGlyGlnArgAlaLeuLysLeuProAsnLeu 368
1100 TGCACATGCTGCTCAGATGCGCTCAGGATGCGGTACGTCGAGCGATG 1149
368 alaSPheAlaIaIaGlnValAlaIaIaGlyMetAlaTyrIleGluArgMet 384
1150 AACTAGTCCACGGGACCTTCTGTCAGAGCAACATCCTGGGAGGAGAA 1199
385 AsnTrpIleHisArgAspLeuArgSerAlaAsnIleLeuValGlyAsnG 401
1200 CCTGGTGTGCAAGTGGCCGACTTTGGCTGGCTGCTCATTGAAGACA 1249
401 yLeuIleCysLysIleHisAspPheGlyLeuAlaArgLeuIleGluAsp 418
1250 ATGAGTACACGGCGCGGCAAGTGCCTCAATCCCATCAAGTGAAGGCT 1299
418 snGluTyrTrpAlaArgGlnGlyAlaLysPheProIleLysTrpThrAla 434
1300 CCAGAGGCTGCGCTTATGGCGCTTACCATCAAGTCAAGTCAAGTGTGCT 1349
435 ProGlnAlaIaIaLeuTyrGlyArgPheThrLysSerAspValTrpSe 451
1350 CTTGCGGATCCTGCTAGTCAAGTCAACACAAAGGAGCGGTCCTACAC 1399
451 rPheGlyIleLeuLeuThrGlnLeuValThrLysGlyArgValProTyrP 468

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1400 CTGGGATGTGAACCGGAGGTCGTGACACGATGAGCGGGGCTACCGG 1449
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485 MetProCysProGlnAspCysProIleSerLeuHisGlnLeuMetIleH 501
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seq_documentation_block:
; Sequence 15, Application US/08426509A
; Patent No. 6326469
; GENERAL INFORMATION:
; APPLICANT: Ullrich, Axel
; APPLICANT: Glisizky, Mikhail
; APPLICANT: Sures, Itman G.
; TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York,
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/426,509A
; FILING DATE: 21-Apr-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/232,545
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7683-0074-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 529 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: No. 6326469e
; US-08-426-509A-15

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Ratio: 4.171          Gaps: 3

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67	easnsersersphrValThThSerProGlnArgAlaGlyProLeuAlaG	84
251	GTGAGTACCAACCTTTGTGGCCCTTATGACTATGAGTCTAGAGCGAG	300
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101	ThraspleuSerPheLysLyselylGluArgLeuGlnIleValAlaAsnTh	117
351	GGAGGAGACACTGGTGGCTGGCGCCACTCGGCTCGACAGACAGACAGCGGT	400
117	rglGluLysprTrpTrpleuAlaHisSerLeuSerThrglyInThrglyT	134
401	ACATGCCCGACACTACGTGGCGCCCTCGACTCCATCCAGGCTGAGAG	450
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551	AAGGTGCTACTGCTCTCAGTGTGTGACTTCGACAGCGCCAAAGGAGC	600
184	ysgIyAlaTyrCysLeuSerValSerAspPheAspAlaLysGlyLeu	200
601	AAGGTGAAGCACTACAGATCCGCAAGCTGGACAGCGGCGGCTTACAT	650
201	AsnValLysHisTyrLysIleArgLysLeuAspSerGlyLysPheTyrI	217
651	CACCTCCCGGACCGAGTTCACAGCGCTGACAGGCTGGTGGCTACTACT	700
217	erThSerArgThrglnPheAsnSerLeuGlnGlnLeuValAlaTyrTyrS	234
701	CGAAACACCGCGAGTGGCTGTGGCACCGCCCTCACACCGGTGGCCCAAG	750
234	erLysHisAlaAspGlyLeuGlyHisArgLeuThrThValCysProThr	250
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251	SerLysProGlnThrGlnGlyLeuAlaLysAspAlaTrpGluIleProAr	267
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267	gglSerLeuArgLeuGlnValAlLysLeuGlyGlnIlyCysPheGlyGluV	284
851	TGTGGATGGGACCTGGAACGGTACACACAGAGTGGCCATCAAAACCTG	900
284	alTrpMetGlyThThrTpsasGlyThrArgValAlaIleLysThrLeu	300
901	AAGCTTGGCAGACGTGTCCAGAGGCTTCTCGACAGAGCGCCAGCTCAT	950
301	LysProGlyThrMetSerProGlnAlaPheLeuGlnGlnAlaGlnValMe	317
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351 AspPheleuylselglutthrglytyrleuAaGleuPheProGlnleuVa 367
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484 eEtrOcyArProProGlnCysProGlnSerIleuHisAsPleuMetCysGln 500
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|||||
1551 CTTCGCGAGGACTACTTCAGCTCCACGAGCGCCAGTACACGCGCCGGGG 1600
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517 aPheleuGlnAsPtyrPheThrSerThGlnProGlnTyrglnProGlyG 534
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|||||
534 luAsnIleu 536

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22-MAR-2000 (first entry)
Wild-type chicken c-Src tyrosine kinase.
Angiogenesis; tyrosine kinase; Src; inhibition; activation; modulate;
chicken; viral expression vector; replication competent; variant Src;
inflammatory disease; arthritis; rheumatoid arthritis; restenosis;
diabetic retinopathy; osteoporosis; cancer.
Gallus sp.
02-DEC-1999

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1401 TGGGATGGGTAACCGGAGGTGCTGACCAAGTGAGACGGGGCTACCGGA 1450
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464 OGlyMetValAsnArgGluValLeuAspGlnValGluArgGlyTyrArgm 481
1451 TGGCCGTCCCGCGGAGTGTCCGAGTCCCTGACAGACACTCATGTGCAG 1500
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481 ePrProCysProProGluCysProGluSerLeuHisAspLeuMetCysGln 497
1501 TGGTGGCGGAGAGAGCCCTGAGAGCGGCCCACTTCGAGTACCTGACAGC 1550
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498 CysTrpArgArgAspProGluGluArgProThrPheGluIleuArgGlnAl 514
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seq_name: /SID51/gcgdata/geneseq/geneseq-emb1/AA2001.DAT: AAB84661
seq_documentation_block:
ID AAB84661 standard; Protein; 533 AA.
AC AAB84661;
DT 05-SEP-2001 (first entry)
XX Amino acid sequence of chicken tyrosine kinase protein Src.
DE
XX
XX Vascular permeability; tyrosine kinase protein; Src; Yes; stroke;
KW myocardial infarction; restenosis; trauma; blood vessel; atherosclerosis;
KW diabetic retinopathy; inflammatory disease; infection; arthritis;
KW adult respiratory distress syndrome; ARDS; rheumatoid arthritis;
KW diabetic retinopathy; psoriasis; neovascular glaucoma;
KW capillary proliferation; osteoporosis; cancer.
XX
XX Gallus sp.
OS
XX
XX WO200145751-A1.
PN
XX
XX 28-JUN-2001.
PD
XX
XX 22-DEC-2000; 2000WO-US35396.
PF
XX
XX 22-DEC-1999; 99US-0470881.
XX 29-MAR-2000; 2000US-0538248.
XX
XX (SCRI) SCRIPPS RES INST.
PA
XX
XX Cheresh DA, Elliceiri B, Paul R;
PI
XX
XX WPI. 2001-417982/44.
DR
XX
XX N-PSDB; AAH28357.
DR
XX
XX Modulating vascular permeability in tissues, including inflamed tissue,
PT tissues associated with stroke, myocardial infarction, by contacting
PT the tissue with tyrosine kinase protein Src, yes or their modified
PT forms
PT
XX
XX
XX Disclosure; Fig 2; 133pp; English.
XX
XX The specification describes a method for modulating vascular
XX permeability in a tissue suffering from a disease condition. The method
XX comprising contacting the tissue with a pharmaceutical composition
XX comprising tyrosine kinase protein Src, yes or their mixtures or
XX nucleic acid expressing them. The method is useful for modulating
XX vascular permeability in tissues, including inflamed tissue, tissues

CC associated with stroke, myocardial infarction or other blockage of
CC normal flow, tissues undergoing restenosis, psoriatic, retinal tissue
CC and similar tissues. Pathologies like may be treated include include
CC trauma to blood vessels, and other systemic pathological events such as
CC atherosclerosis, diabetic retinopathy, inflammatory disease due to
CC infection by microbial agents and arthritis. Other diseases which can
CC be treated include adult respiratory distress syndrome (ARDS), rheumatoid
CC arthritis, diabetic retinopathy, psoriasis, neovascular glaucoma,
CC capillary proliferation in atherosclerotic plaques and osteoporosis and
CC cancer associated disorders such as solid tumours, solid tumour
CC metastases, angiodiomas and hemangiomas. The present sequence
CC represents chicken Src, and is used in the method of the invention.
XX
XX
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Ratio: 5.112 Gaps: 1
Percent Similarity: 97.201 Percent Identity: 94.030
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101 CCTGCAGACCCCGCAGCAAGCCAGCTGCGCGAGCGGCGGCGCC 150
|||||
31 lAserGlnThrProAsnLysThrAlaAlaProAspThrHisArgThrPro 47
151 AGCGCGCGCTTGGCGCGCGCGCGCGCGCGCAAGCTGTGGAGGCTT 200
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48 SerArgSerPheGlyThrValAlaThrGluProLysLeuPheGlyGly 64
201 CAATCCTCGGACACCGTCACTCCCGCGAGAGGCGGCGCGCGTGGCG 250
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64 eAsnThrSerAspThrValThrSerProGlnArgLysAlaLeuAlaG 81
251 GTGAGTGCACCACTTGTGGCCCTATGACTATGACTAGAGCGAG 300
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81 lGlyValThrThrPheValAlaLeuTyrAspTyrGluSerArgThrGlu 97
301 ACAAGCTGTCTTCAAGAAAGCGAGCGGCTCCAGATTGCAACACAC 350
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98 ThrAspLeuSerPheLysLysGlyLysArgLeuGlnIleValAsnAsn 114
351 GGAGGAGAGACTGTGGCGCGCGCACTCGCAGACAGAGAGAGGCT 400
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114 rGluGlyAspTrpTrpLeuAlaHisSerLeuThrThrLysGlnThrGly 131
401 ACATCCCGCAGCACTAGTGGCGCGCTCCGACTCATCAGAGCTAGAG 450
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131 yTlleProSerAsnTyrValAlaProSerAspSerIleGlnAlaGluGlu 147
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501 TGCAGAGAACCGGAGAGGAGGAGCTCCGTCGCGAAGAACTAGACCA 550
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164 nProGluAsnProArgGlyThrPheLeuValArgGluSerGluThrTr 181
551 AAGTGGCTACTGCTCTCACTGTCTGACTCGACAGCGCAAGGCGCTC 600
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 Ratio: 5.105 Gaps: 1
 Percent Similarity: 97.201 Percent Identity: 93.843

Alignment block:

US-09-444-711-1 x AAY44449

Align seg 1/1 to: AAY44449 from: 1 to: 533

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17  rLeuGlnProProAspSerThrHis.....HisGlyGlyPhePro 31
101  CCTGCGACAGCCCGACCAAGCCCTGCGCGCGCGCGCGCGCGCGCC 150
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31  lAserGlnThrProAsnLysThrAlaAlaProAspThrHisArgThrPro 47
151  AGCGGGCGCTTGGCCCCCGCGCGCGCGCGCGCGCGCGCGCGCGCTT 200
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48  SerArgSerPheGlyThrValAlaThrGlnProLysLeuPheGlyGlyPh 64
201  CAATCTCTCGACACCGTCACCTCCCGCGAGAGGGCGCGCGCGCGCGCG 250
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64  eAsnThrSerAspThrValThrSerProGlnArgAlaGlyAlaAlaG 81
251  GTGGAGTACACACTTGTGGCCCTCTATGACTATGAGTCTAGAGAGGAG 300
  |||||ValThrThrPheValAlaLeuTyAspTyrGlnSerArgThrGln 97
81  LyGlyValThrThrPheValAlaLeuTyAspTyrGlnSerArgThrGln 97
301  ACAGACCTGCTCTTCAAGAAAGCGAGCGCGCTCCAGATTGTCAACACAC 350
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98  ThrAspLeuSerPheLysLysGlyLysArgLeuGlnLLeValAlaAsnsmth 114
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214  ethSerArgThrGlnPheSerSerLeuGlnGlnLeuValAlaTyrTyrS 231
701  CCAAGACGCGGATGGCTGTGCCAGCGCTCAACACCGGTGGCGCCACG 750
  |||||erLysHisAlaAspGlyLeuLysHisArgLeuThrAsnValCysProThr 247
231  erLysHisAlaAspGlyLeuLysHisArgLeuThrAsnValCysProThr 247
751  TCCAGGCGGACAGACTCAGGCGCTGCGCAAGATGCTGGAGAGATCCCTCG 800
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281  AlrPheMetGlyThrTyrAsnGlyThrThrArgValAlaAlaLysThrLeu 297
901  AAGCTGGACAGATGTCTCCAGAGGCTTCTCGACGAGGCGCCAGCTCAT 950
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951  GAAGAGCTGAGGACATGAGAAGCTGGTGGCAGTGTATGCTGTGCTTACG 1000
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331  GlnLLeuProLLeuTyrLLeuValThrGlnLLeuTyrMetSerLysGlySerLeu 347
1051  GACTTCTCAAGGGGAGACAGGCAAGTACCTGCGGCTGCTCAGCTGCT 1100
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414  nGlnTyrThrAlaArgGlnGlyAlaLysPheProLLeuTyrPheThrAla 431
1301  CAGAACTGCGCTCTATGCGCGCTTACCATCAAGTCGAGCGTGGTCTC 1350
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431  roGlnAlaAlaLeuTyrGlyArgPheThrLLeuLysSerAspValTyrPse 447
1351  TTCGGATCCTGCTGACTGAGCTCACACACAAAGGAGGCGTGGCTTACCC 1400
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481  eCProLysProProGlnLysProGlnSerLeuHisAspLeuMetCysGln 497
1501  TGCCTGGCGAAGAGAGCTGAGAGCGCGCCACCTTGAGTACTGAGAGC 1550
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498  CysTyrPheArgArgAspProGlnGlnArgProThrPheGlnTyrLeuGlnAl 514
1551  CTTCCTGGAGGACTACTTACGTCACCGACGAGCGCCAGTACACAGCCCGGG 1600
  |||||||aPheLeuGlnAspTyrPheThrSerThrGlnProGlnPheGlnProGlyG 531
514  aPheLeuGlnAspTyrPheThrSerThrGlnProGlnPheGlnProGlyG 531
1601  AGAACCTC 1608
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 ID AAR39705 standard; Protein: 533 AA.
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1201 CTGGTGTGCAAGTGGCCGACTTTGGGTGGCGGTGGCTGCTATTGAAGACAA 1250
1252 |||||||
414 ngUuTyTrpAlaArgGlnGIyAlaIysPheProIleTyStrpThrAlaP 431
1301 CAGAACCTGCGCCCTCTATGGCGCGCTTCACCATCAAGCGGACGCTGTC 1350
1351 |||||||
431 roGIuAlaAlaLeuTyrgIyArgPheThrIleIysSerAspAlaTrpSer 447
1351 TTCGGGATCCTGCTGACTGAGCTCACACAAAGGAGCGGCTGCTACCC 1400
1448 PheGIyIleIleuLeuThrGluLeuThrIleTyrgIyArgValProIyTr 464
1401 TGGGATGTGTGAACCGCGAGGTGCTGGACCAAGGTGAGCGGGGCTACCGA 1450
1464 |||||||
464 oGIyMetValAsnArgGIuValIleuAspGlnValGIuArgGIyTYrArgM 481
1451 TGGCCCGCCCGCGGAGTGTCGCCGATCCCTCGACAGACTCATGTGCCAG 1500
481 ecTrpCysProProGIuGlyCysProGIuSerIleuHisAspIleuMetCysGln 497
1501 TCCTGGCGGAGAGGAGCCTGAGGAGCGGCCACCTTGATGACTGAGAGCG 1550
498 CysTrpArgArgAspProGIuGluArgProIleuArgPheGIuTyrgIleuGlnAl 514
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seq_name: /SIDS1/gcdata/geneseq/geneseq_emb1/AA2000.DAT:AA44451
seq_documentation_block:
ID AA44451 standard; Protein: 533 AA.
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AC
AY44451;
XX
22-MAR-2000 (first entry)
XX
Mutant chicken c-Src tyrosine kinase, Src(K295M).
XX
Angiogenesis; tyrosine kinase; Src; inhibition; activation; modulate
KM chicken; mutant; Src(K295M); point mutation; tumor cell signalling;
AV binding; proliferation; kinase domain; inflammatory disease; can
os osteoporosis; rheumatoid arthritis; diabetic retinopathy; restenosis
XX
Gallus sp.
OS
Synthetic.
XX
Key Location/Qualifiers
FT Misc-difference 295 /label=K295M
FT /note="Wild type Lys replaced with Met"
XX
W09961590-A1.
XX
02-DEC-1999.
XX
28-MAY-1999; 99WO-US11760.
XX
29-MAY-1998; 98US-0087220.
XX

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(SCRI) S C R I P P S R E S I N S T .
Cheresh DA, Elliceiri B, Schwartzberg PL;
WPI; 2000-116335/10.
using tyrosine kinase Src for modulating angiogenesis in tissues useful
in, e.g. treatment of chronic articular rheumatism -
Claim 6; Page -: 80pp; English.

The present sequence is the mutant chicken c-Src tyrosine kinase,
Src(K295M). This sequence has a point mutation, K295M, in the kinase
domain, which prevents ATP binding and also blocks kinase dependent
Src functions related to vascular cell and tumour cell signalling and
proliferation. This mutant Src(K295M) protein, can be used to modulate
specifically inhibit angiogenesis. When the Src protein is inactivated,
angiogenesis is inhibited while, when it is activated, angiogenesis is
potentiated. The mutant or variant Src can be used to treat inflammatory
diseases like, arthritis, rheumatoid arthritis, diabetic retinopathy,
restenosis, osteoporosis and cancer associated disorders.
Note: This sequence is not found in the specification, but derived
from the sequence in Fig 2.

alignment_scores:	Quality: 2657.50	Length: 536
	Ratio: 5.111	Gaps: 1
Percent Similarity:	97.015	Percent Identity: 93.843

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alignment_block:
US-09-444-711-1 x AAAY44451 ..
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[illegible]

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151 ProLeuTyrIleValThrGluTyrMetSerYsglySerLeuLeuAsp 167
1056 TCTCAAGGGGAGAGACAGCAAGTACCTGGCGGCTCCACAGCTGGTGACA 1105
167 eLeuYsglyGluThrGlyLysTyrLeuNrgLeuProGlnLeuValAsp 184
1106 TGGCTGCTCAGATCCGCTCAGGCTGCGGTACGTGAGCGGATGAACTAC 1155
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1156 GTCCACCGGAGACTGTGTGACGCAACATCCTGTGTGGAGAGAACCTG 1205
201 ValHISArgAspLeuNrgAlaIleAlaAsnIleLeuValGlyLysLeuVal 217
1206 GTGCAAGGGGCGGAGTGTGGCTGGCTGGCTGCTGCTGCTGCTGCTGCT 1255
217 lGysYsglyValAlaAspPheGlyLeuAlaTyrLeuIleGlnAspAsnGlu 234
1256 ACACGGCGGCGGAGAGTGGCAATTCCTCCATCAAGTGGAGCGGTCAGAA 1305
234 YrThrAlaTyrGlnGlyAlaLysPheProIleLysThrAlaProGlu 250
1306 GCTGCCCTATGAGCGCTTACCATCAATGTCGAGCTGTGCTGCTGCTG 1355
251 AlaAlaLeuTyrGlyArgPheThrIleLysSerAspValTrpSerPheG 267
1356 GATCCTGCTGAGTACGACCAACAAGGAGCGGTGCTTACCTGAGGA 1405
267 YrLeuLeuThrGlnLeuThrThrLysGlyArgValProTyrProGly 284
1406 TGGTAGACGCGAGTGTGAGACGAGTGGAGCGGCTACCGGATGCC 1455
284 eValAlaAsnTrpGlnValLeuAspGlnValGlnArgGlyTyrArgMetPro 300
1456 TGCCTCCGCGAGTGTCCGAGTCCCTGACAGCTCATGTGCGGAGCTG 1505
301 CysProProGluCysProGluSerLeuHISAspLeuMetCysGlnCys 317
1506 GCGGAGGAGCCTGAGAGAGCGGCCACTTCAGTACCTGACAGCCTTCC 1555
317 pArgLysGlnProGluGlnArgProThrPheGluTyrLeuGlnAlaPhe 334
1556 TGGAGATCACTTACAGTCCACGAGCCCGGATACAGAGCCCGGAGAAC 1605
334 eGlnLysPyrThrPheThrSerThrGlnProGlnTyrGlnProGlyGlnAsn 350
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seq_name: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT: AAB99332
seq_documentation_block:
ID AAB99332 standard; Protein: 505 AA.
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AC AAB99332;
XX
DT 23-AUG-2001 (first entry)
XX
DE Human tyrosine kinase Hck protein sequence SEQ ID NO:11.
XX
KW Human; tyrosine kinase Hck binding protein; tyrosine kinase; Hck;
KW tumour lethal factor; tumour necrosis factor alpha; apoptosis; HSB-1;
KW Hck signal transduction; human immunodeficiency virus; HIV infection;
KW anticancer.
XX

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OS Homo sapiens.
XX
XX WO200132869-A1.
XX
PD 10-MAY-2001.
XX
XX 26-OCT-2000; 2000WO-JP07500.
XX
XX 29-OCT-1999; 99JP-0309957.
XX
XX (SSSE) SSP CO LTD.
XX
XX Tanigawa T, Narita T;
XX
DR WPI; 2001-316440/33.
XX
XX
XX New proteins which bind to human tyrosine kinase Hck for promotion of
XX apoptosis and for the elucidation of the mechanism of Hck signal
XX transduction
XX
XX Example 1; Page 33-35; 45pp; Japanese.
XX
XX The present invention describes a protein, designated HSB-1, which binds
XX to human tyrosine kinase Hck. Also described are: (1) nucleic acids
XX encoding the protein and its derivatives; (2) recombinant vectors
XX containing the nucleic acids; and (3) host cells transformed by the
XX vectors and expressing the protein. HSB-1 has cytostatic activity, binds
XX tyrosine kinase, enhances tumour necrosis factor alpha and promotes
XX apoptosis. HSB-1 proteins are used for the elucidation of the mechanism
XX of Hck signal transduction and of the role of Hck in human
XX immunodeficiency virus (HIV) infection. They can be used for the
XX treatment of infections and other diseases with which Hck is associated.
XX They promote the anticancer activity of tumour necrosis factor alpha.
XX The present sequence represents the human tyrosine kinase Hck protein,
XX which is used in an example from the present invention.
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XX Sequence 505 AA:
XX
XX
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XX Quality: 1526.00 Length: 511
XX Ratio: 3.731 Gaps: 7
XX Percent Similarity: 80.039 Percent Identity: 58.121
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XX 125 .....CCTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTTGC 163
XX 28 roValTyrValProAspProThrSerThrIleLysProGly...Prosn 43
XX 164 CCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 213
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531 luInleu 533

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seq_documentation_block:
: Sequence 14, Application US/08426509A
: Patent No. 6326469
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: GENERAL INFORMATION:
: APPLICANT: Ulrich, Axel
: APPLICANT: Gishizsky, Mikhail
: APPLICANT: Sures, Irman G.
: TITLE OF INVENTION: NOVEL MEKAKARYOCYTIC PROTEIN
: TITLE OF INVENTION: TYROSINE KINASES
: NUMBER OF SEQUENCES: 21
: CORRESPONDENCE ADDRESS:
: ADDRESS: Pennie & Edmonds
: STREET: 1155 Avenue of the Americas
: CITY: New York,
: STATE: NY
: COUNTRY: USA
: ZIP: 10036-2711
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/426,509A
: FILING DATE: 21-APR-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/232,545
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Coruzzi, Laura A
: REGISTRATION NUMBER: 30,742
: REFERENCE/DOCKET NUMBER: 7683-0074-999
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212-790-9090
: TELEFAX: 212-869-9741
: TELEX: 66141 PENNIE
: INFORMATION FOR SEQ ID NO: 14:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 543 amino acids
: TYPE: amino acid
: STRANDEDNESS: unknown
: TOPOLOGY: unknown
: MOLECULE TYPE: No. 6326469e
: US-08-426-509A-14

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seq_documentation_block:
; Sequence 12, Application US/08426509A
; Patent No. 6326469
; GENERAL INFORMATION:
; APPLICANT: Gillich, Axel
; APPLICANT: Gliszky, Mikhail
; APPLICANT: Sures, Irman G.
; TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York,
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/426,509A
; FILING DATE: 21-Apr-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/232,545
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7683-0074-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141 PENNIE

```


APPLICANT: United States of America
 APPLICANT: Missenachafen E.V.
 APPLICANT: Hofgarten Str. 2
 APPLICANT: Munchen 80539
 APPLICANT: Germany
 TITLE OF INVENTION: Novel Megakaryocytic Protein Tyrosine
 NUMBER OF INVENTION: Kinases
 NUMBER OF SEQUENCES: 21
 CORRESPONDENCE ADDRESS:
 ADDRESSER: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/05008
 FILING DATE: 24-Apr-1995
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/232,545
 FILING DATE: 22-Apr-1994
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Coruzzi, Laura A.
 REGISTRATION NUMBER: 30,742
 REFERENCE/DOCKET NUMBER: 7683-074
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212)790-9090
 TELEFAX: (212)869-9741
 TELEEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 536 amino acids
 TYPE: amino acid
 STRANDEDNESS: unknown
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 PCT-US95-05008-13

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 Quality: 2834.00 Length: 536
 Ratio: 5.287 Gaps: 0
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67 eaenSerSerAspThrValThrSerProGlnArgAlaGlyProLeuAlaG 84
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 84 LysGlyValThrThrPheValAlaLeuLysAspTyrGluSerArgThrGlu 100
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 101 ThrAspLeuSerPheLysLysGlyLysGluArgLeuGlnLeuValAsnThr 117
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 117 rGluGlyAspTyrThrPheLeuAlaHisSerLeuSerThrGlyGlnThrGly 134
 401 ACATCCCGCAACACTACGTGGCGCGCTCGACACTCCATCCAGGCTGAG 450
 134 YrileProSerAsnTyrValAlaProSerAspSerIleGlnAlaGluGlu 150
 451 TGCTATTGTCGCAAGATCACACAGCGGAGTCAAGGGTACTGCTCAA 500
 151 TrpTyrPheGlyLysIleThrArgArgGluSerGlnArgLeuLeuAs 167
 501 TGCAGAGAACCCGAGAGGAGCTTCCTCGTGCAGAAAGTGAACACGA 550
 167 nAlaGluAsnProArgGlyThrPheLeuValArgLysSerGlnThrThrL 184
 551 AAGTGCTACTGCTCTCAAGTGTGACTTGCACAACGCCAGAGGCGCTC 600
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 201 AsnValLysHisTyrLysIleArgLysLeuAspSerLysGlyPheTyr 217
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 217 eThrSerArgThrGlnPheAsnSerLeuGlnGlnLeuValAlaTyrTyr 234
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 234 eLysHisAlaAspGlyLeuCysHisArgLeuThrThrValCysProThr 250
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 301 LysProGlyThrMetSerProGluAlaPheLeuGlnGlnAlaGlnValMe 317
 951 GAAGAAGCTGAGGATGAGAAGCTGGTGCAGTTGATGCTGTTGTTGAG 1000
 317 TLysLysLeuArgHisGluLysLeuValGlnLeuTyrAlaValIleSerG 334
 1001 AGAGCCCATTTACATGTCACGAGTACATGACAGAGGAGGAGTTGCTG 1050
 334 LgluLysProIleTyrIleValThrGlnLysMetSerLysGlySerLeuLeu 350
 1051 GACTTTTCAAGGGGAGAGACAGGCAAGTACCTGGCGCTCAGCTGTG 1100
 351 AspPheLeuLysGlyGluThrGlyLysTyrLeuArgLeuProGlnLeuVa 367
 1101 GGAATGGCTGCTCAGATCCGCTCAGGATGCGCTAGGTGAGGAGGAGA 1150


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Db 781 GATCCTGGGATCCCTCCGGGAGTGGTGGGAGGTCMACTGGCGGAGGCTGC 840
Qy 841 ttggcagagtggtgagtgagtgagtgagtgagtgagtgagtgagtgagtgag 900
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Db 1201 CTGGTGTGCAAAAGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1260
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Db 1501 TGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1560
Qy 1561 gactactcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1611
Db 1561 GACTACTTCAGCTCCAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1611

```

RESULT 3
US-07-820-011A-1

Sequence 1, Application US/07820011A
Patent No. 533615

GENERAL INFORMATION:

APPLICANT: Bell, Leonard

APPLICANT: Madri, Joseph A.

APPLICANT: Warren, Stephen L.

APPLICANT: Lutheringer, Daniel J.

TITLE OF INVENTION: Genetically Engineered
TITLE OF INVENTION: Endothelial Cells Exhibiting Enhanced
TITLE OF INVENTION: Migration
TITLE OF INVENTION: and Plasminogen Activator Activity

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:
ADDRESSEE: Maurice M. Klee
STREET: 1951 Burr Street

```

CITY: Fairfield
STATE: Connecticut
COUNTRY: USA
ZIP: 06430
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb storage
OPERATING SYSTEM: IBM PC XT
SOFTWARE: Displaywrite 3
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/820,011A
FILING DATE: 19920106
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Klee, Maurice M.
REGISTRATION NUMBER: 30,399
REFERENCE/DOCKET NUMBER: LB-101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 255 1400
TELEFAX: (203) 254 1101
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1602 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: Double
TOPOLOGY: Linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Gallus, gallus
PUBLICATION INFORMATION:
AUTHORS: Takeya, Tatsuo
AUTHORS: Hanafusa, Hidesaburo
TITLE: Structure and Sequence of the
TITLE: Cellular Gene Homologous to the RSV src
TITLE: Gene and the Mechanism for Generating the
TITLE: Transforming Virus
JOURNAL: Cell
VOLUME: 32
PAGES: 881-890
DATE: March, 1983
US-07-820-011A-1

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Query Match 75.5%; Score 1216.6; DB 1; Length 1602;
Best Local Similarity 85.2%; Pred. No. 5.9e-238;
Matches 1373; Conservative 0; Mismatches 229; Indels 9; Gaps 1;

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Qy 61 gccgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 120
Db 61 CCCGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 111
Qy 121 ccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 180
Db 112 ACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 171
Qy 181 ccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 240
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Db 232 GCATGAGCTGGCGGGGTACACACTTTCGTGGCTCTACGAGTACGAGTCCCGACTGAA 291
Qy 301 acagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 360
Db 292 ACGGAGCTTGTCTTCAAAAGAGAGAGAGCGCTGCGAGATTTGTAACACAGCAGAGGTGAC 351

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1 PUBLICATION INFORMATION:
 2 AUTHORS: Anderson, Stephen K.
 3 AUTHORS: Gibbs, Carol P.
 4 AUTHORS: Tanaka, Akio
 5 AUTHORS: Kung, Hsing-Jien
 6 AUTHORS: Fujita, Donald J.
 7 TITLE: Human Cellular src Gene:
 8 TITLE: Nucleotide Sequence and Derived Amino
 9 TITLE: Acid Sequence of the Region Coding for
 10 TITLE: The Carboxy-Terminal Two-Thirds of
 11 TITLE: pp60c-src
 12 JOURNAL: Molecular and Cellular Biology
 13 VOLUME: 5
 14 ISSUE: 5
 15 PAGES: 1122-1129
 16 DATE: May, 1985
 17 PUBLICATION INFORMATION:
 18 AUTHORS: Tanaka, Akio
 19 AUTHORS: Gibbs, Carol P.
 20 AUTHORS: Arthur, Richard R.
 21 AUTHORS: Anderson, Stephen K.
 22 AUTHORS: Kung, Hsing-Jien
 23 AUTHORS: Fujita, Donald J.
 24 TITLE: DNA Sequence Encoding the
 25 TITLE: Amino-Terminal Region of the Human c-src
 26 TITLE: Protein: Implications of Sequence
 27 TITLE: Divergence among src-Type Kinase
 28 TITLE: Oncogenes
 29 JOURNAL: Molecular and Cellular Biology
 30 VOLUME: 7
 31 ISSUE: 5
 32 PAGES: 1978-1983
 33 DATE: May, 1987
 34 US-07-820-011A-3

Query Match	99.9%	Score 1609.4	DB 1	Length 1611
Best Local Similarity	99.9%	Pred. No. 0		
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QY	121	ccaagcctcgtgcagacgagcaacggtgcgcacagcgcgagccttcgcgcccgcgccgag	180
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QY	181	cccaagctgttcctgcgagccttcaactcctcgcgacacgctcaccctccgcgagaggtgc	240
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QY	241	ccggtgtgcgcgttgagatgtagcacaactttgtgtgcctctatgatagtactagacgag	300
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QY	301	acagacactgtctctccaagaaagacgagcgcgtccagattgtctcacaacaacgagagggac	360
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QY	361	tgtgtgtgtgcgcccaactcgctcagcacaagacagagctacatccccaacatacgtg	420
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QY	421	ggcgccctccgcctccatccacagcgtgcagagatgtgattttgacaagatccacaacgagag	480
Db	421	ggcgccctccgcctccatccatccacagcgtgcagagatgtgattttgacaagatccacaacgagag	480
QY	481	tcagagacggttactgtctcaatgcagagaaaccgcgagaggaacctctcgtgtgcgagaagt	540

Db	481	TCAGACGCGTTACTGCTCAATGCAAGAGAACCCGAGAGGAGCACTTCTCGTGCAGAAAGT	540
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QY	601	aagctgaagcactacaagaatccgcgaagctgtgacaacgagcgcgctctcatcacctccgc	660
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QY	661	accagattcaaacagcctgcagaagcctggttgctactactccaacacgcccgtatgctgt	720
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Db	901	AAGCCTCGGACAAATGTCCTCCAGAGGCTTCTCAGAGAGCCCAAGGTCTATGAAGAACTTG	960
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QY	1141	gagcgagtatgaactacgttccacccggagaccttcgtgcacccaacactcctgtgtggagagaac	1200
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QY	1441	ggcttcacgaatccctcggcccgccgagagtgtcccgagttcccttgacaagaccctcatgtccag	1500
Db	1441	GGCTTACGATCCCTCGGCCCGCGGAGTGTCCGAGTCTCTTGACGACCTCTATGTGGCAG	1500
QY	1501	tgtctgagaaagagcctctagagagcgccacaaccttgatgaactctgagagcctccctgtgag	1560
Db	1501	TGCTTGCGAAGAGAGCCTTAGAGAGCGGCCCACTTGTGAGTACTGCAAGGCTTCTCTGTGAG	1560
QY	1561	gactacttaagttcacagagcccaagtaaccaagcccgggagaaactctag 1611	

Sequence 4517 BP; 1437 A; 784 C; 955 G; 1341 T; 0 other:

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Query Match      44.1%; Score 710.2; DB 22; Length 4517;
Best Local Similarity 70.1%; Pred. No. 6.9e-125;
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OY 308 tgcctctcaagaagcgagcggtccagattgtlcaacaacacaggaagagagctgtgtgc 367
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OY 368 tggcccaactgcctcagcacaggaagacagactacatccccaagaactactgtgcgcct 427
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DB 656 cagattccattcagcgaggaagaatgtatttggcaaaatggggggaagaagaatgtctgaa 715
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OY 488 ggttactgtcctaattgcagagaaccccgagagagaccttctgtgcgagaaagttagacca 547
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DB 716 gattactttgataatcccggaatcaacgaggtatttcttaagtagagaggtgaacaa 775
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OY 548 cgaaggtgctactactgcctcctcagtgctgtgactgcgaacacgcaagggctcaactga 607
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OY 608 agcaactacaagaatccggaagctgagcgagcggtcttataacgctccgaccccgact 667
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OY 668 tcaacagcctgcagcagactgtgtgctactactcaacaacgcgagtgctgtgcacc 727
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DB 1076 aagtgtagtagggagacatgtagtaaacacagaaagtgcacatcaaacactaaacag 1135
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OY 908 gcacgatgtctcagagagcttctcgcagagagccaggtcatgaaagaagctgagcatg 967
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DB 1136 gtacaatgatgcgaagaacttctcctcaagaagctcagataatgaaaaataagaacatg 1195
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OY 968 agaaagctgggagcatgttatgtctgtgtttagaggagcccatatacctgtcaagagat 1027
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DB 1196 ataactgttccacataatgtctgttcttgaagaacacattacatgtccactgcat 1255
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OY 1028 acatgacgaagggaggtttgtgtagcttctcacaagggggaacagcagcagctgcggc 1087
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DB 1256 ttatgtcaaaaagaagcttataattccttaaggaagagatggaagatatttgaagc 1315
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OY 1088 tgcctcagctgtgtgaacatgctcagatcgcctcagatgcgcatggtcgtgtagcgga 1147
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DB 1316 ttccacagctgttgatagtgctgtcagattgtcgtgatgcatatataatagaaga 1375
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OY 1148 tgaactacgtccacggagacttctgtgacccaacatcctgtgtggaagaacgtgtgt 1207
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OY 1208 gcaagtgccgagacttgggtgtgtgtcgtcgaatggaacacatagtaacagggcgcg 1267
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DB 1436 gcaaaatagcagacttggtttagcaaggttaattgaagaacaatgaatacagaagac 1495
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DB 1496 aaggtgcaaaatttcccaactgaatgtagacgtctccgaagctgcgaattgtatgtgtta 1555
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 1328 ccatcaagtgcgaagctgtgtctcctcggatcctgtcgtactgtgagctcaccacaaggag 1387
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1556 caataaagtctgactgtctgtcatttggatattctgtcaacagaactagttaacaaggcgc 1615
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 1388 ggtgtgctaccctcggatgtgtgaacccgaggtgtgtgagcaggtgtgagcggtcctc 1447
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1616 gagtgcatactccagtgatgtgtgaacccgtgaagtaactgaagaatgtgagagatata 1675
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 1448 gtagtgcctgcgcgcgagtggtcccgatccctgcagacactcatgtgccagtgtgcg 1507
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1676 ggtatgcgtgctcccaaggtcgttcagataatccctcagaattgtatgtatcgtgtgga 1735
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 1508 ggaagagcctgagagagcgccacactcagatcgtcagagccttctcgtgagactact 1567
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1736 agaagagacctgtatgaagacacattgtaatatattcagctccttctgtgaagactact 1795
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 1568 tcaagtccacagagcccaagtaaccagcccggtggaacactcta 1610
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1796 tcactgtcacagagccacagtaaccagccaggaagaattata 1838
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 11
AAS74489
ID AAS74489 standard; CDNA: 4517 BP.
XX
AC AAS74489;
XX
DN 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #10293.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
XX
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI: 2001-639362/73.
XX
DR P-PSDB: ABG10302.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity -
XX
PS Claim 1; SEQ ID NO 10293; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX and gene mapping, and in recombinant production of (II). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX (II). (II) is useful for generating antibodies against it, detecting or
```

[illegible]

XX	Human yest encoding cDNA.
XX	Human yest; diagnosis; neuropsychiatric disorder; BAD; schizophrenia;
XX	bipolar affective disorder; attention deficit disorder;
XX	schizoaffective disorder; unipolar affective disorder;
XX	Huntington's disease; Parkinson's disease; manic-depression; ss.
XX	
OS	Homo sapiens.
XX	
XX	Key
XX	Location/Qualifiers
XX	208..1839
XX	CDS
XX	/*tag= a
XX	
XX	W09935290-A1.
XX	
XX	15-JUL-1999.
XX	
XX	07-JAN-1999; 99WO-US00297.
XX	
XX	08-JAN-1998; 98US-0003944.
XX	
XX	(MILL-) MILLENNIUM PHARM INC.
XX	
XX	Chen H, Freimer NB;
XX	
XX	WPI; 1999-444203/37.
XX	
XX	P-PSDB; RAY24421.
XX	
XX	Detection of a genetic mutation in the yest gene, useful for
XX	diagnosis of a yest mediated neuropsychiatric disorder in a human
XX	
XX	Disclosure; Fig 1; 110pp; English.
XX	
XX	The present invention describes a method for detecting a genetic
XX	mutation in the yest gene for the diagnosis of a yest mediated
XX	neuropsychiatric disorder in a human. The method comprises detecting the
XX	presence or absence of a genetic mutation in the yest gene of the
XX	subject, where the genetic mutation is a substitution, insertion or a
XX	deletion and results in the production of a yest protein having an amino
XX	acid sequence other than the wild-type yest amino acid sequence and the
XX	presence of the genetic mutation identifies a subject that has or is at
XX	risk for developing a yest mediated neuropsychiatric disorder. Compounds
XX	that bind to the yest protein, alter the amount of the protein, or alter
XX	the activity of the yest gene product, are useful for treating a yest
XX	mediated neuropsychiatric disorder. The disorders include Huntington's
XX	disease, Parkinson's disease, and especially bipolar-affective disorder
XX	(BAD) also known as bipolar mood disorder (BP) or manic-depressive
XX	illness. The method distinguishes neuropsychiatric disorders from
XX	neurological disorders, which enables more accurate evaluation and
XX	prescription of medical treatment. The present sequence represents the
XX	human yest cDNA sequence.
XX	
XX	Sequence 4517 BP; 1431 A; 781 C; 952 G; 1340 T; 13 other;
XX	
XX	Query Match 44.1%; Score 710.2; DB 20; Length 4517;
XX	Best Local Similarity 70.1%; Pred. No. 6.9e-125;
XX	Matches 955; Conservative 0; Mismatches 408; Indels 0; Gaps 0;
XX	
XX	248 ccggtgagatgacacaccttggccctctatgactatgagtcgtgacgagacagacc 307
XX	
XX	476 caggtggtctactattatgtgctctatattgattatgaagctaacataagaagacc 535
XX	
XX	308 tgccttaagaagaagcgagcggtcccgatgttaacaacscgggaaggaagctgtggc 367
XX	
XX	536 ttctattagaagaagggtgaagaattccaataatacgaagaagatgtgtg 595
XX	
XX	368 tggccactgcctcgcacagacagacagacgtacatcccccgaactacgtggcgccct 427
XX	
XX	596 aagcaagatcaatcgctacacggaagaagtgttatatcccgagcaatattgtagcgctg 655
XX	
XX	428 ccgactcatccaggtcgaggaatgtgattttggcaagataccacagcggaatcagagc 487

Db	823	tgccacacgcctgacacaaagctctgcgcacacagtcacaaagccacagacacacaggaattctgcacaa	882
Oy	781	gattccctcggagaaatccctctcggagagtcgcgtctcgagctctgagagtgacagctgggacagggctgc	840
Db	883	gacgcgcggagaaatccccccgggagagtcgcgtcgcgcctcgagagctggagagctgggacagggctgc	942
Oy	841	ttctggcagagctgttgatctggggagacctggaaacggtacacacagaggtgtggcatcaaaaacctg	900
Db	943	ttctggagagagctctgtagtattgggagaccttggaacgcgcacacacagagagtggtgcataaagaacctg	1002
Oy	901	aagcctctcggacagatgtctccacagagggctctctctcgcacagagggcccaagctcatgaagaagctg	960
Db	1003	aagcctcggagacacatgtctcccgagggagctctctctcgcacagagaaagcccaagctgtagaagagctc	1062
Oy	961	aggcactgagaaagctggctgacagttgtatgtctgtgtgtttcacaagagagcccatltaacatgctc	1020
Db	1063	cggcagtagaagctgtgtcttcagctgtacgcagctgtgtctcgaaagagcccatctaacctgc	1122
Oy	1021	acggagagtaacatgacagcaaggggagagtttgcgtggacctcttcacaaggggagagcaagctac	1080
Db	1123	actgtagtaacatgacagagggagagcctctctgtgaattctctgaaagggagagagagagagctac	1182
Oy	1081	ctgcgcgcctcccaagctctgtctgagacagagcgtgcctcagatcgcacagcccaagctgagcgtaagtg	1140
Db	1183	ctgcgcgcctcccaagctctgcctcgtatagctgtgcctcagatgtcatctcgcgcacagctgtaagtg	1242
Oy	1141	ggcgcgagatgaactacgtctccacccggagacctctgcgcagcccaacactcctggctggggagagaa	1200
Db	1243	ggagagagatgaactacgtctccacccggagacctctgcgcagcccaacactcctggctggggagagaa	1302
Oy	1201	ctgtgtgtgcacaaagtggccgaccttttggctggctgcgtgcgcgtcatctgaaagacaaatgagtaacg	1260
Db	1303	ctgtgtgtgcacaaagtggctgcgtaccttttggctggctgcgcgtcatctcagagagacagtagtacaa	1362
Oy	1261	ggcgcgcgcacaggtgtgcacaaattccccaacagtgagagcgctcccaagagctgcacctataagc	1320
Db	1363	ggacgcgcgcacaggtgtgcacaaattccccaacagtgagagcgcccccagagcagcaccctataagc	1422
Oy	1321	ggcttcacacatcaagctcgagacgtgtgtctctcgggagatcctgtcagactgagctcagaca	1380
Db	1423	ggcttcacacatcaagctcgagatgtctgtcctctcgacactctgtcgtactgtgactgtgacacac	1482
Oy	1381	aagggacgggtgtccctaccaccttggagatgtgaaccgcgcagaggtgtcctggagacagagtgagacg	1440
Db	1483	aagggacgggtgtccctaccacagagatgtgtacaacagagaggtgtcctggagacagagtgagagag	1542
Oy	1441	ggctacacggatgcccctgc	1500
Db	1543	ggctacacggatgcccctgc	1602
Oy	1501	tgctgcgcgaaagagcctcggagagcgcgccaccctctgagtagactcggagcgccttcctgag	1560
Db	1603	tgctgcgcgaaagagcctcggagagcgcgccaccctttgagtagactcggagcgccttcctgag	1662
Oy	1561	gaactactcaagctccacgcgagcccccagttaccagccgcgggagaaacctctag	1611
Db	1663	gaactactcaagctccgcacagagcccccagttaccagccgcgtgagagaaacctatag	1713
RESULT 5			
AA046687			
ID AA046687 standard; cDNA to mRNA; 1602 BP.			
AC AA046687;			
XX 23-DEC-1993 (first entry)			
DT Chicken pp60 c-src gene.			
XX Endothelial; tyrosine kinase protein; pp60 c-src; ss.			
XX Gallus gallus.			
XX			

PM W09314193-A.
 XX 22-JUL-1993.
 PD
 XX
 PF 05-JAN-1993; 93WO-US000445.
 XX
 PR 06-JAN-1992; 92US-0820011.
 XX
 PA (UYTA) UNIV YALE.
 XX
 PI Bell L, Luthringer DJ, Madri JA, Warren SL;
 DR WPI; 1993-243209/30.
 DR P-PSDB; AAR39705.
 XX
 PT Genetically engineered endothelial cells - which exhibit enhanced
 PT cell migration, urokinase-type plasminogen activator activity,
 PT and reduced mononuclear cell adhesion and fibronectin prodn
 XX
 XX Disclosure; Page 59-62; 91pp; English.
 PS
 CC The DNA encoding a portion or (more preferably) the entire p60
 CC c-src polypeptide is used to transform endothelial cells.
 CC Transformed cells produce increased amounts of p60 c-src and have
 CC improved therapeutic properties. They migrate at faster rates than
 CC non-transformed counterparts; have an enhanced ability to inhibit
 CC the formation of thrombi and/or dissolve thrombi once they have
 CC formed and exhibit reduced mononuclear cell adhesion. They can al
 CC be used to improve the success of surgical procedures such as
 CC coronary angioplasty, heart bypass surgery, vessel graft and stent
 CC implantation.
 CC
 SQ Sequence 1602 BP; 350 A; 503 C; 481 G; 268 T; 0 other;

[illegible]

RESULT 3

AA229700
ID AA229700 standard; cDNA; 1759 BP.

AC AA229700;

DT 22-MAR-2000 (first entry)

DE Wild-type chicken c-Src tyrosine kinase cDNA.

XX Angiogenesis; tyrosine kinase; Src; inhibition; activation; modulate;
XX chicken; viral expression vector; replication competent; variant Src;
XX inflammatory disease; arthritis; rheumatoid arthritis; restenosis;
XX diabetic retinopathy; osteoporosis; cancer; ss.

OS Gallus sp.

XX Key Location/Qualifiers

FT CDS 112..1713
FT /tag- a
FT /product- "Chicken c-Src tyrosine kinase"

FT /note- "Src used to modulate angiogenesis"

XX MO961590-A1.

XX 02-DEC-1999.

XX 28-MAY-1999; 99MO-US11780.

XX 29-MAY-1998; 98US-0087220.

XX (SCRI) SCRIPPS RES INST.

XX Chersesh DA, Elliceiri B, Schwartzberg PL;

XX WPI: 2000-116335/10.

XX P-PSDB; AAY44447.

XX Using tyrosine kinase Src for modulating angiogenesis in tissues useful
XX in, e.g. treatment of chronic articular rheumatism -

XX PS Claim 1; Fig 1; 80pp; English.

XX The present sequence is the cDNA, encoding the wild-type chicken c-Src
XX tyrosine kinase. This sequence encoding the Src protein, can be used to
XX modulate angiogenesis. When the Src protein is inactivated, angiogenesis
XX is inhibited, while when it is activated, angiogenesis is potentiated.
XX The modified or variant Src can be used to treat inflammatory diseases
XX like, arthritis, rheumatoid arthritis, diabetic retinopathy, restenosis,
XX osteoporosis and cancer associated disorders.

XX Sequence 1759 BP; 370 A; 554 C; 533 G; 302 T; 0 other;

Query Match 75.6%; Score 1218.2; DB 21; Length 1759;
Best Local Similarity 85.3%; Pred. No. 1.4e-220;
Matches 1374; Conservative 0; Mismatches 228; Indels 9; Gaps 1;

QY 1 atgggtgcaacaagcaagcccaagatgacagccagcgccgacgagcttgagacc 60
DB 112 atggggagcgacgaagcaagcccaagacccagcgccgagcagcttgagacca 171
QY 61 gccagagacgtgacgagcgctgagcgagcttcccgagcttcagaccgccgaag 120
DB 172 ccgagacgacccacacac-----ggggattccagcagcttcgacacccacacag 222
QY 121 ccagcctcgagcgagccagcgccagcgagccttcgcccgcgagcgagcgag 180
DB 223 acagcagcccccagacgacgacccacccagcgcctcttgagacgtgagcagcgag 282
QY 181 ccaagactgttcgagagcttaactcctcgacacgcgtcaacctcccgagagggcgagc 240

DB 283 cccaagctcttcgggggttcacacactcttgacacccgttgcgcgagcgttcgcgg 342
QY 241 ccgctgagccgtgtgagtgaccaccttctgagccctctatgactatgactagagcgag 300
DB 343 gcaactgagcgtgagcgttcacacacttctgagctctctatgactagcagcgcgagctgaa 402
QY 301 acagacccgtctcttaagaagaagcgagcgctccagatctgtcaacaacgagagagac 360
DB 403 acgagactgtctctcaagaagaagagacgcctgcagatgttcaacaacacggaagtgac 462
QY 361 tgggtgagccagcttcagcagcagagcagagcagagctatcccgacgacatcgtg 420
DB 463 tgggtgagccagcttcagcagcagagcagagcagagcagagctatcccgacgacatcgtg 522
QY 421 ggcgcctccagatccatccagcagctgagagtgatatttgacagatcacacagcgagag 480
DB 523 ggcgcctccagatccatccagcagctgagagtgatatttgacagatcacacagcgagag 582
QY 481 tcagagcggttactgtctcaatgcaagagaccgagagagaccttcgtgcgagaaat 540
DB 583 tccgagcggtctgtctcaaccccgaaaaccccgaggagacacttctgtccgggagagc 642
QY 541 gagaccacgaaaggtgctcactgtccttcagtgctcagtgcttcgacacgccaagggcctc 600
DB 643 gagacacaaaaggtgctcactgtccttcagtgctcagtgcttcgacacgccaagggcctc 702
QY 601 aacgtgaagcactatacagatccgacagctgacagcgagcggtcttctacacccctccgc 660
DB 703 aatgtgaagcactatacagatccgacagctgacagcgagcggtcttctacacccctccgc 762
QY 661 accagatcaacagcctgacagcagctgtgtgcttactactcaacaacgacgagtgctg 720
DB 763 acacagttcagcagcctgacagcagctgtgtgcttactactcaacaacgagtgctgctg 822
QY 721 tgcacccgctcaccacacgctgtgcccacagtcgacagcgacagctcagggcccgacag 780
DB 823 tgcacccgctcaccacacgctgtgcccacagtcgacagcgacagctcagggcccgacag 882
QY 781 gatgcctgggaatccctcgcgagctgcgtcgctgtgaggtcaagcttgagccagcgctgc 840
DB 883 gacggtgtggaatccctcgcgagctgcgtcgctgtgaggtcaagcttgagccagcgctgc 942
QY 841 ttgtgagaggtgtgagtgagagcctggaacgttacccaagaggtgtgcatcaaacctgc 900
DB 943 ttgtgagaggtgtgagtgagagcctggaacgttacccaagaggtgtgcatcaaacctgc 1002
QY 901 aagcttgacagatgtccccaagccttcctgcagagcgagagccaggttcataagagctg 960
DB 1003 aagcccgacacatgtccccaagccttcctgcagagcgagagccaggttcataagagctg 1062
QY 961 aggcattgagaaactgtgtcagatgtatgctgtgttcagagagagccattcatcgtgc 1020
DB 1063 cggcatgtgaaactgtgtcagatgtatgctgtgtgttcagagagagccattcatcgtgc 1122
QY 1021 acgagatcatgagcaagggaggttctgtgacattctcaagggggagacagcaagtlac 1080
DB 1123 actgagatcatgagcaagggaggttctgtgacattctcaagggggagacagcaagtlac 1182
QY 1081 ctgcgagctgcctcaactgtgtgagtgagtgctgtgagtgagtgagtgagtgagtg 1140
DB 1183 ctgcgagctgcctcaactgtgtgagtgagtgctgtgagtgagtgagtgagtgagtgag 1242
QY 1141 gagcgatgaatacgttccacgagacactctgtgcagccaacatccctgtgtgagagagac 1200
DB 1243 gagagatgaatacgttccacgagacactctgtgcagccaacatccctgtgtgagagagac 1302
QY 1201 ctgtgtgtcnaaagtgtgcagacttctgtgctgcgttcattgaagacaaatgaatcacg 1260
DB 1303 ctgtgtgtcnaaagtgtgcagacttctgtgctgcgttcattgaagacaaatgaatcacg 1362
QY 1261 ggcggcnaaagtgtgcagacttcccatcaagtgagcgtcccaagagctgcctctatgac 1320

XX Disclosure; Page 69-72; 91pp; English.

CC The DNA encoding a portion or (more preferably) the entire pp60
CC c-src polypeptide is used to transform endothelial cells.
CC Transformed cells produce increased amounts of pp60 c-src and have
CC improved therapeutic properties. They migrate at faster rates than
CC non-transformed counterparts; have an enhanced ability to inhibit
CC the formation of thrombi and/or dissolve thrombi once they have
CC formed and exhibit reduced mononuclear cell adhesion. They can also
CC be used to improve the success of surgical procedures such as
CC coronary angioplasty, heart bypass surgery, vessel graft and stent
CC implantation.

SD Sequence 1611 BP; 334 A; 507 C; 504 G; 266 T; 0 other;

Query Match	99.9%	Score 1609.4	DB 14	Length 1611
Best Local Similarity	99.9%	Pred. No. 2.9e-294		
Matches 1610; Conservative	0	Mismatches 1	Indels 0	Gaps 0

QY	1	atggtgtatgcacaagaagagcacaagaagatctgcacagccaagcgctgcagacccctctgcagccc	60
QY	1	atgggtatgcacaagaagagcacaagaagatctgcacagccaagcgctgcagacccctctgcagccc	60
QY	61	gcccagagacgtgcacagcgctctgcagcgagcgcttcccccgcctccgcagagaccccacagaag	120
Db	61	gcccagagacgtgcacagcgctctgcagcgagcgcttcccccgcctccgcagagaccccacagaag	120
QY	121	ccagacctctgcagcgacgagccacgcgcgcacagcgctcttcgcaccccccgcgcgcgcagag	180
Db	121	ccagacctctgcagcgacgagccacgcgcgcacagcgctcttcgcaccccccgcgcgcgcagag	180
QY	181	cccaagaagtgttcgagagagcttccaaactcctctcgagacaacgctacaccccccgcagagcgcgac	240
Db	181	cccaagaagtgttcgagagagcttccaaactcctctcgagacaacgctacaccccccgcagagcgcgac	240
QY	241	ccgcctgcgcgcgttcgagagcgacacaccttctgtgcctcctatgactatgactatgagcagagag	300
Db	241	ccgcctgcgcgcgttcgagagcgacacaccttctgtgcctcctatgactatgactatgagcagagag	300
QY	301	acagaaacctgtctccttcacaagaaagcgagcgagctccagaattgttcacaacaacaagagggagagac	360
Db	301	acagaaacctgtctccttcacaagaaagcgagcgagctccagaattgttcacaacaacaagagggagagac	360
QY	361	tgtgtgtgtgtgcgcacactctgcctcagcacaagcgacagaacaggtacatcccccagcaactcgtgcg	420
Db	361	tgtgtgtgtgtgcgcacactctgcctcagcacaagcgacagaacaggtacatcccccagcaactcgtgcg	420
QY	421	ggcgccctccagactccatccacaagcgctcgagagagttgttatcttgcaagatcacacagaacgagag	480
Db	421	ggcgccctccagactccatccacaagcgctcgagagagttgttatcttgcaagatcacacagaacgagag	480
QY	481	tcaaagacggttactgtctcctcaatctgcagagaaacccgagagagaccttccctctgcgcgcgcagaaagt	540
Db	481	tcaaagacggttactgtctcctcaatctgcagagaaacccgagagagaccttccctctgcgcgcgcagaaagt	540
QY	541	gagagccacgaaaaggtgtgctactctgtcctctcaggtgtctcgaacttcgacaacgcccgaagggcttc	600
Db	541	gagagccacgaaaaggtgtgctactctgtcctctcaggtgtctcgaacttcgacaacgcccgaagggcttc	600
QY	601	aaacgttgaagacattacaagaatccgcgaagcttggaacgctgcgcgtcttctacatccacatccctccgcg	660
Db	601	aaacgttgaagacattacaagaatccgcgaagcttggaacgctgcgcgtcttctacatccacatccctccgcg	660
QY	661	accacagttcaacagcctctgcagacgctgtgtgtgctactactccacaacagcgcgagtgcgtcgtg	720
Db	661	accacagttcaacagcctctgcagacgctgtgtgtgctactactccacaacagcgcgagtgcgtcgtg	720
QY	721	tgcacacgcgtctacacacacgctgtgcgccacgcttcaacgcccgaagcctgaagcctgcgcgcag	780
Db	721	tgcacacgcgtctacacacacgctgtgcgccacgcttcaacgcccgaagcctgaagcctgcgcgcag	780

QY	761	gataccctcggagagatcccttcctcggagctcggctcggagctcggagctgaagctaaactcggccagagctcgc	840
Db	761	gattccctcggagagatcccttcctcggagctcggctcggagctcggagctgaagctaaactcggccagagctcgc	840
QY	841	cttcgcgagagctcgtcgaagcggagacctcggaaacgtgtacaaccaagagctgtgcacatacaaaacctcg	900
Db	841	cttcgcgagagctcgtcgaagcggagacctcggaaacgtgtacaaccaagagctgtgcacatacaaaacctcg	900
QY	901	aagccctgcagacgatagtctcctcagaagagcccttcctcgaagagagccccaaggtcatagaagaactcg	960
Db	901	aagccctgcagacgatagtctcctcagaagagcccttcctcgaagagagccccaaggtcatagaagaagctcg	960
QY	961	agggacataagaaagctcgtgcagctgtcgtatcgtctgtgtcttcacagagagagcccaatactaatcgtc	1020
Db	961	agggacataagaaagctcgtgcagctgtcgtatcgtctgtgtcttcacagagagagcccaatactaatcgtc	1020
QY	1021	acggagatcataagataagacaaagggagatcttcgtcgaactcttcataaggggagagacaaagctaac	1080
Db	1021	acggagatcataagataagacaaagggagatcttcgtcgaactcttcataaggggagagacaaagctaac	1080
QY	1081	ctcgcgcgtcgcctcagcctcgtcgtcgaacatcgtcgtcacaagatccgcctcagaagcagatcggctgaacg	1140
Db	1081	ctcgcgcgtcgcctcagcctcgtcgtcgaacatcgtcgtcacaagatccgcctcagaagcagatcggctgaacg	1140
QY	1141	gagcgcgagatgaactcactgtccacacggagaccttcgtgcagcccaacatcctgtgtcggagagaaac	1200
Db	1141	gagcgcgagatgaactcactgtccacacggagaccttcgtgcagcccaacatcctgtgtcggagagaaac	1200
QY	1201	ctggctgtgcacaagatgggcgcgaactcttcggcctcggcctcatatgaagacaatagaataacag	1260
Db	1201	ctggctgtgcacaagatgggcgcgaactcttcggcctcggcctcatatgaagacaatagaataacag	1260
QY	1261	gcgcgcgcgaagatgtgcacaattccccaatacaagctgaagcgcgtccacagaagctcgcctcctaatgac	1320
Db	1261	gcgcgcgcgaagatgtgcacaattccccaatacaagctgaagcgcgtccacagaagctcgcctcctaatgac	1320
QY	1321	cgcctcacatcaatgaatcgcgaagctgtgtgtctcttcggagatccctcgtgaactcgtacatgcatacaca	1380
Db	1321	cgcctcacatcaatgaatcgcgaagctgtgtgtctcttcggagatccctcgtgaactcgtacatgcatacaca	1380
QY	1381	aaggagacggatgtgcctcctaccccttcggatgagtcgagaaacggagagctcgtgacaagaatgtgagacgg	1440
Db	1381	aaggagacggatgtgcctcctaccccttcggatgagtcgagaaacggagagctcgtgacaagaatgtgagacgg	1440
QY	1441	ggctcacacggatgcctcctcgcgcggcggagatgtcccgagctccctgcacagacctaactcatgtgcag	1500
Db	1441	ggctcacacggatgcctcctcgcgcggcggagatgtcccgagctccctgcacagacctaactcatgtgcag	1500
QY	1501	tgctcgcgcgagaaagagcctcgtcgaagcgcgcgcacacacttcggagatcaactcgtcagaagccttcctcgag	1560
Db	1501	tgctcgcgcgagaaagagcctcgtcgaagcgcgcgcacacacttcggagatcaactcgtcagaagccttcctcgag	1560
QY	1561	gactactctcaactcaccacagagccccaagtacacagcccgaggagagaaactctag	1611
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RESULT ' 2			
AA587965	AA587965 standard; cDNA; 1699 BP.		
ID	AA587965 standard; cDNA; 1699 BP.		
XX	AA587965;		
XX	13-FEB-2002 (first entry)		
DE	DNA encoding novel human diagnostic protein #23769.		
KV	Human; chromosome mapping; gene mapping; gene therapy; forensic;		
KX	food supplement; medical imaging; diagnostic; genetic disorder; ss.		
OS	Homo sapiens.		
PN	MO200175067-A2.		

401 ACATCCCGAGAACTAGCTGGCGCCCTCCGACTCCATCCAGGCTGAGAG 450
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131 yrileProserAsnTyrlaValaProserAspSerlleGlnalaeIuGlu 147
451 TGGATTTTGGCAAGATCACAGAGCGGAGTACAGCGGCTTACTGCTCAA 500
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148 TrpTrpHeGlyLyslleThrArgArgIuSerGluArgLeuLeuAs 164
501 TGCAGAGAACCCGAGAGGACCTCTCTGTCGAGAAAGTAGAGACACGA 550
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164 nProGluAsnProArgIuThrPheLeuValArgIuSerGluThrPrl 181
551 AAGTGCCCTACCTGCTCAGTGTCTGACTTCGACACGCCAAGGCGCTC 600
|||||
181 ysgIaIaTyrcysLeuSerValSerAspPheAsnAlaLysIleu 197
601 AACGTGAAGCACTACAGATCCGCAAGCTGGACAGCGCGGCTTACAT 650
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198 AsnValLysHisTyrlaArgIuLysLeuAspSerGlyGlyPheTyrl 214
651 CACCTCCCGACCCAGTTCAACAGCCTGACAGCTGGTGGCTTACTACT 700
|||||
214 eThSerArgThrGlnPheSerSerleuGlnGlnValaIaTyrlTyrS 231
701 CCAAAACAGCCGATGCGCTGTGCCACCGCTCACCCCGCTGTGCCACG 750
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231 eTyrSHisAlaAspGlyLeuTySHisArgLeuThrAsnValCysProThr 247
751 TCCAGCCGCGAGACTCAGGGCTGGCCCAAGATGCTGGAGATCCCTCG 800
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248 SerLysProGlnThrGlnGlyLeuAlaLysAspAlaTrpGluLeuProAr 264
801 GGAGTCCCTGGGGCTGGGTCAGAGCTGGCGGCTGCTTGGCCGAG 850
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264 gEluSerLeuArgLeuGlnValLysLeuGlyGlnLysPheGlyGlu 281
851 TGTGATGGGACCTGGAACGGTACACCAAGGTGGCCATCAAAACCTG 900
|||||
281 alTrpMetGlyThrTrpAsnGlyThrArgValaAlaIleLysThrIeu 297
901 AAGCTGGCAGATGTCTCCAGAGGCTTCTGACGAGGCCAGGCTCAT 950
|||||
298 LysProGlyThrMetSerProGluAlaPheLeuGlnGlnAlaGlnValMe 314
951 GAAGAAGCTGAGCATGAGAGCTGTCGATGTCATGCTGCTGTTGAG 1000
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314 TLyLysLeuArgHisGlnLysLeuValGlnLeuTyrlaValaValaSer 331
1001 AGGAGCCCATTTACATGCTGACGAGATGATGAGCAAGGGAGTTGGTG 1050
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331 IuGluProIleTyrlleValaThrGluTyrlMetSerLysGlySerLeuLeu 347
1051 GACTTTCTCAAGGGGAGACAGCAAGTACCTGCGGCTGCTCAGCTGT 1100
|||||
348 AspPheLeuLysGlyGluMetGlyLysTyrlLeuArgLeuProGlnIeuVal 364
1101 GGAATGGCTCTCAGATGCGCTCAGGATGGCGTACGTGAGCGGATGA 1150
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364 IAspMetAlaIaGlnIleAlaSerGlyMetAlaTyrlaValaGlnArgMetAla 381
1151 ACTAGCTCCACCGGAGCTGCTGTCGACCAACATGCTGGTGAGAGAAC 1200
|||||
381 snTyrlValHisArgAspLeuArgAlaAlaAsnIleLeuValaLysIuAsn 397
1201 CTGGTGTCAAAAGTGGCGACTTTGGCTGGCTGCGCTCATTTGAAGACA 1250
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398 LeuValaLysLysValaAlaAspPheGlyLeuAlaArgLeuIleGluAspAs 414
1251 TGAATACAGCGCGGCAAGGTGCCAAATTCCTCAATCAAGTGGAGCGCTC 1300
|||||
414 nGluTyrlThrAlaArgGlnGlyAlaLysPheProIleLysTrpThrAlaP 431
1301 CAGAAGCTGCCCTCTATGGCGGCTTCACACATCAAACTCGAGCTGTGGTCC 1350

|||||
431 roGluAlaIaLeuTyrlGlyArgPheThrIleLysSerAspValTrpSer 447
1351 TTCGGATCCCTGCTGACTGAGCTCACACCAAGAGGAGGCTGCCATACC 1400
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448 PheGlyIleLeuLeuThrGlnLeuThrIleLysGlyArgValaProTyrr 464
1401 TGGATGTGAACCGGAGAGTCTGAGACCAAGGTGAGCGGGGCTTACCGA 1450
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464 ocIlyMetValaAsnArgGluValLeuAspGlnValaGlnArgGlyTyrlArg 481
1451 TGCCCTGCCCGCGGAGTGTCCGAGTCCCTGACAGCTCATGTGCCAG 1500
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481 eLProCysProProGluCysProGluSerLeuHisAspLeuMetCysGln 497
1501 TGCTGGCGGAAGAGCTTACGCTGACGTCACGAGCCGCTTGCAGTACCTGACGC 1550
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498 CysTrpArgArgAspProGluGlnArgProThrPheGluTyrlLeuGlnAl 514
1551 CTTCCTGGAGAGACTTCTACGCTCCACGAGCCGCTGACAGCCGAGG 1600
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514 aPheLeuGluAspTyrlPheThrSerThrGluProGluTyrlGlnProGly 531
1601 AGAACCTC 1608
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531 LuAsnLeu 533

seq.name: /cgn2_6/ptodata/1/1aa/PCITUS_COMB.pep:PCT-US93-00445-2

seq_documentation_block:
: Sequence 2, Application PC/TUS9300445
: GENERAL INFORMATION:
: APPLICANT: Bell, Leonard
: APPLICANT: Madri, Joseph A.
: APPLICANT: Warren, Stephen L.
: APPLICANT: Luthinger, Daniel J.
: TITLE OF INVENTION: Genetically Engineered
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Maurice M. Klee
: STREET: 1951 Burr Street
: CITY: Fairfield
: STATE: Connecticut
: COUNTRY: USA
: ZIP: 06430
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch, 760 Kb storage
: COMPUTER: DELL 486/50
: OPERATING SYSTEM: DOS 5.0
: SOFTWARE: Displaywrite 3
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US93/00445
: FILING DATE: 19930105
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/820,011
: FILING DATE: 06-JAN-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Klee, Maurice M.
: REGISTRATION NUMBER: 30,399
: REFERENCE/DOCKET NUMBER: ALX-101PCT
: TELEPHONE: (203) 255 1400
: TELEFAX: (203) 254 1101
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 533 amino acids
: TYPE: AMINO ACID
: TOPOLOGY: Linear
: MOLECULE TYPE: Protein
: HYPOTHETICAL: NO
: FRAGMENT TYPE: Complete Sequence

